

STIC Database Tracking Number:

TO: Cynthia Wilder Location: Rem 2a35

Thursday, February 12, 2004

Art Unit: 1637 Phone: 272-0791

Serial Number: 09 / 981606

From: Jan Delaval

Location: Biotech-Chem Library

Rem 1A51

Phone: 272-2504

jan.delaval@uspto.gov

Search Notes



STIC-Biotech/ChemLib

13949

From:

Chan, Christina

Sent:

Tuesday, February 10, 2004 9:23 AM Wilder, Cynthia; STIC-Biotech/ChemLib

To: Subject: RE: Rush sequence search for 09/981606

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

----Original Message----

From:

Wilder, Cynthia

Sent:

Tuesday, February 10, 2004 9:09 AM

To:

Chan, Christina

Subject:

Rush sequence search for 09/981606

Ms. Chan,

I am requesting a rush sequence search and for interference of the following: 09981606. This case needs prompt attention.

Please forward your approval to STIC

Please provide a search of nucleotides 67-339 of SEQ ID NO: 1, wherein at position 193 and A is substituted for a T.

Please provide a search of nucleotides 700-850 of SEQ ID NO: 1, wherein a mutation is located at nucleotide 845.

Please provide a search of nucleotides 4652-4915 and nucleotides 6494-6927 of SEQ ID NO: 27.

Thank you

Cynthia B. Wilder, Ph. D.

United States Patent and Irade Mark Office
Carlyle Remson 2035
(571) 272-0791

2 C | 8

Searcher: Phone:	22504
Location: Date Picked Up:	2/10
Date Completed: Searcher Prep/Revie Clerical:	
Online time:	-7W

TYPE OF SEARCH:	
NA Sequences:	
AA Sequences:	
Structures:	
Bibliographic:	
Litigation:	_
Full text:	
Patent Family:	
Othor	

VENDOR/COST (W	here applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	·
Sequence Sys.:	
www/Internet:_	
Other (specify):_	

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Sequence 10, Appli
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                                                                                     February 11, 2004, 15:39:52 ; Search time 49.5778 Seconds
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/SB_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/RB_COMB.seq:*

(cgn2_6/ptodata/1/ina/RB_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-834-497A-9
US-08-834-497A-19
US-09-503-444A-10
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US-09-503-444A-3
US-09-652-265-3
US-08-724-394A-22
US-08-724-394A-22
US-08-652-265-7
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Maximum Match 100%
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                                                             - nucleic search, using sw model
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ALIGNMENTS

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APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEGUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAREATIN Release #1.0, Version #1.30

SOFTWARE: PAREATIN Release #1.0, Version #1.30

SURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,265

FILING DATE: 23-MAY-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: SMith, William M.

REGISTRATION NUMBER: 17957-000500

TELEPHONE: (415) 576-0200

TELEFANTION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1440 base pairs

TOPOLOGY: linear

MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Bighth Floor
           ; Sequence 9, Application US/08652265; Patent No. 6025130; GENERAL INFORMATION:
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222..1268
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STATE: California
COUNTRY: USA
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LOCATION: replace
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LOCATION:
FEATURE:
US-08-652-265-9
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99.4%; Score 271.4; DB 3; Length 1440;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0;
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APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   /phenotype= "normal or wild-type
(unaffected)"
/label= 24d1
/phenotype= "normal or wild-type (unaffected)".
/label= 24d2
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                                                                                                                                                                                                     /phenotype= "nc
(unaffected)"
/label= 24d7
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                                                                                                                                            NAME/KEY: allele
LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: /label= 24
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: (label= 24)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OP INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS: 76
CORRESPONDENCE ADDRESS: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1440;
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99.4%; Score 271.4; DB 3;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1;
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           E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 9, Application US/08834497A; Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                     LOCATION: replace (1066, "a")
OTHER INFORMATION: /phenotype=
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
Smith, William M.
                                                                                                                                                              LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                 CDS
222..1268
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: New York
                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                        NAME/KEY; allele
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APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Gairke, Andreas
APPLICANT: Haddy, David
APPLICANT: Thuchinashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
COCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: EastSED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFTCATION 514
PROR APPLICATION DATA:
FILING DATE: 23-MAY-1996
CLASSIFTCATION: 514
                                                                                                                               528 recactarrarecaaarcacaccacacacacac
                                                                                    241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Pennie & Edmonds LLP
T: 1155 Avenue of the Americas
New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION MUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         Sequence 10, Application US/08834497A Patent No. 6140305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 890
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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10036-2811
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                                                                                                                                                                                                                                                    US-08-834-497A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: N
STATE:
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99.4%; Score 271.4; DB 3; Length 1440;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indel8 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /phenotype= "normal or wild-type (unaffected)" |
| label= 24d2
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                        OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSON for Windows Version 2.0b
CURRENT APPLICATION DATA:
PRPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: US 08/632,673
PRIOR APPLICATION 514
PRIOR APPLICATION 514
PRIOR APPLICATION 514
PRIOR APPLICATION 514
PRIOR APPLICATION: 514
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-4935
TELEFAX: 650-493-556
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OTHER INFORMATION: /phenoty
OTHER INFORMATION: (unaffect
OTHER INFORMATION: /label=
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OTHER INFORMATION: /phenoty
OTHER INFORMATION: (unaffec
OTHER INFORMATION: /label=
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 222..1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
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121 CAIGAGIGICGCCGIGIGGAGCCCCGAACTCCAATGCAGTAGAATTTCAAGCCAG 180
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APPLICANT: Thomas, Dennis T.
APPLICANT: Beder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
ITLE CANT: Wolff, Roger K.
ITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                             /phenotype= "normal or wild-type
(unaffected)"
/label= 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                       /phenotype= "normal or wild-type
(unaffected)"
/label= 24d7
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99.4%; Score 271.4; DB 3;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Patent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: replace(414, "a")
OTHER INFORMATION: /phenoty
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                                                                                                                                                                                                                                                                                                LOCATION: replace (408, "COTHER INFORMATION: (phem) OTHER INFORMATION: (unaficility of the INFORMATION: /labe: FEATURE: NAME/KEY: allele
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 herry
                                                                                          1440 base pairs
                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 222..1268
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                             1 CGCTTGCTGCGTTCACACTCTTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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0
                                                                         Query Match
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09503444A
; Sequence 9, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
    APPLICANT: Thomas, Winston J.
    APPLICANT: Feder, John N.
    APPLICANT: Gnirke, Andreas
    APPLICANT: Gravid, David
    APPLICANT: Tsuchihashi, Zenta
    APPLICANT: Wolff, Roger K.
    TITLE OF INVENTION: Hereditary Hemochromatosis Gene
    NUMBER OF SEQUENCES: 44
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGACTATTATGGAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 redacratraredaaaarcacaaccacadcaag 560
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMINICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLAING DAILS: 14 TED-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY AGENT INFORMATION:
                 ; OTHER INFORMATION: /label= 24dl
US-08-834-497A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-503-444A-9
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Sequence 1, Application US/09679729

Sequence 1, Application US/09679729

FREERI NO. 6509442:

APPLICANT: Rothenberg, Barry E.

APPLICANT: Barton, James C.

TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS

FILE REPERRENCE: 24065-004 DIV

CURRENT PAPLICATION NUMBER: US/09/679,729

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2506

TYPE: DNA

CORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 271.4; DB 4; Length 2506;
Pred. No. 6e-82;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                      APPLICANT: Rotherdy, Barry E.
APPLICANT: Rotherdy, Barry E.
APPLICANT: Sawada-Hirai, Ritsuko
APPLICANT: Sawada-Hirai, Ritsuko
APPLICANT: Barron, James C.
TITLE OF INVENTION: MITAITONS ASSOCIATED WITH IRON DISORDERS
FILE REFERENCE: 10653/002001
CURRENT APPLICATION NUMBER: US/09/277,457
CURRENT FILING DATE: 1999-03-26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (0)...(0); OTHER INFORMATION: Missense mutation at nucleotide 314 US-09-277-457-1
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                                                                                  US-09-277-457-1
; Sequence 1, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.4%;
Best Local Similarity 99.6%;
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
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NAME/KEY: mutation
LOCATION: (0)...(0)
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LENGTH: 2506
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PURISH APPLICATION NUMBER:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/62,265
FILING DATE: 12-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
RECOMMUNICATION INFORMATION:
TELEPHONE: 212-969-9741
: 1155 Avenue of the Americas
New York
New York
                                                                                                                                                                                                   ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: WordPerfect Version 8
CURRENT APPLICATION DATA:
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LOCATION: replace(1066, "a")
COTHER INFORMATION: /phenotype=
OTHER INFORMATION: /label= 24dl
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 272; Conserv
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LOCATION:
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NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                   222..1268
NAME/KEY: CDS
LOCATION: 222..126
FEATURE:
NAME/KEY: allele
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US-08-652-265-12
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                                                                                             Gaps
                                                                                           0;
                                                      Length 2506;
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APPLICANT: Incure.
APPLICANT: Feder, John N.
APPLICANT: Reder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Herchitash;
APPLICANT: Herchitash;
APPLICANT: Herchitash;
APPLICANT: Herchitash;
APPLICANT: Herchitary Hemochromatosis Gene
                                                      Score 271.4; DB 4; Length 2
Pred. No. 6e-82;
0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 17957-000500
TELEPHONE: (415) 576-0200
TELEPAK: (415) 576-0200
TELEPAK: (415) 576-0300
TELEPAK: CHANSACTERISTICS:
SEQUENCE CHARACTERISTICS:
 ; OTHER INFORMATION: Missense mutation at nucleotide 314 US-09-679-729-1
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Two Embarcadero Center, Eighth Floor
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
                                                        99.4%;
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                                                          Query Match
Best Local Similarity 99.6
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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California
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                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                              0,
                                                                                                                                                                     Query Match
98.8%; Score 269.8; DB 3; Length 1440;
Best Local Similarity 99.3%; Pred. No. 1.6e-81;
Matches 271; Conservative 0; Mismatches 2; Indels 0;
| LOCATION: replace(408, "g") | COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d2 | COTHER INFORMATION: /label= 24d2 | US-08-652-265-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKFT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Dredr, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Finbarcadero Center, Eighth Floor STRY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08652265 Patent No. 6025130 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 175
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FastSEQ for Windows Version 2.0b
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-834-497A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
Local Similarity 99.3%; Pred. No. 1.6e-81;
Los 271; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                         /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                               /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08834497A, Patent No. 6140306; GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                    /label= 24d1
                                                                                                                                                                                                                                                                                  /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY F
                                                                                                                                                                                                                                                                                                                                      LOCATION: replace (1066, "a")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: /label= 24
US-08-652-265-12
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                      LOCATION: replace (408, "g")
OTHER INFORMATION: /phenotyl
OTHER INFORMATION: /label= ::
FEATURE:
                          LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                              CDS
222..1268
                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
                                                                                                                                                                                                        NAME/KEY: allele
                                                                                      linear
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ZIP: 10036-2811
                                                                                    TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                              NAME/KEY:
LOCATION:
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Matches
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121 CATGAGTGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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LOCATION: replace(408, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 24d2
OTHER INFORMATION: /label= 24d2
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Pred. No. 1.6e-81;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: US 08/632,673
APPLICATION NUMBER: US 08/632,673
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION 514
PRIOR APPLICATION 514
PRIOR APPLICATION S14
PRIOR APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.3%;
Matches 271; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650-493-493:
TELERAX: 650-493-5556
TELEX: 66141 PENUE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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181 AIGIGGCIGCAGCIGAGICAGAGICTGAAAGGGTGGGATCACAIGITCACIGITGACTIC 240
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                           188 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347
                                                                                                       61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
                                                                                                                                                 408 GATGAGAGTCGCCGGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467
                                                                                                                                                                                                                                                                                                                                                  468 AIGIGGCTGCAGCTGAGTCAGAGTCTGAAAGGTGGGGATCACATGTTCACTGTTGACTTC 527
CGCTTGCTGCGCTTCACACTCTTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KESULT 13
US-09-503-444A-11
Sequence 11, Application US/09503444A
| Patent No. 622894
| Patent No. 622894
| Patent No. 622894
| Patent No. 622894
| APPLICANT: Thomas, Winston J. APPLICANT: Thomas, Winston J. APPLICANT: APPLICANT: Ruddy, David APPLICANT: Ruddy, David APPLICANT: Wolff, Roger K. TITLE OF INVENTION: Hereditary Hemochromatosis Gene NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS: Abonds LLP STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
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SUCTRARE:
WORDSTEEL VETSION
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
PROOR APPLICATION DATA:
PROOR APPLICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PRIOR DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | COCATION: replace (1066, "a") | COCATION: replace (1066, "a") | OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d1 | US-08-834-497A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: replace (408, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d2
                                                                                      APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                     STATE: New York
SUMPRY: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC comparible
OPERATING SYSTEM: Windows 95
SOFTWARE: FRRESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/652,265
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
CLASSIFICATION 514
PRIOR APPLICATION 514
PRIOR APPLICATION 514
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICALLC.
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 89.07-0056-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
           Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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EDNESS: single
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222..1268
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NAME/KEY: allele
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NAME/KEY: allele
LOCATION: replace
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Best Local Similarity
Matches 271; Conserv
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NAME/KEY:
LOCATION:
           APPLICANT:
APPLICANT:
APPLICANT:
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 ATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527
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                                                                                                                                                                                                                                                                   Length 1440;
                                                                                                                                       LOCATION: replace(408, "g")

TOTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                                                                          Indels
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APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
AUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                            Query Match
98.8%; Score 269.8; DB 3
Best Local Similarity 99.3%; Pred. No. 1.6e-81;
Matches 271; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                528 TGGACTATTATGGAAAATCACAACCACAGGAAG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09503444A Patent No: 6228594 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23.May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                          CDS
222..1268
                 MOLECULE TYPE: CDNA
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: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-503-444A-12
                                                                                                                     NAME/KEY:
LOCATION:
                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                            US-09-503-444A-11
TOPOLOGY:
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288 cecrrecrecerreacacrererecacracererreareserecereasascasearerr 347
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LOCATION: replace(1066, "a")
LOCATION: replace(1066, "a")
OTHER INFORMATION:
OTHER INFORMATION: /label= 24di
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Pred. No. 1.6e-81;
0; Mismatches 2; Indels
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                                                                                                                                                                8907-0088-999
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                                              08/630,912
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FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,91
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INPORMATION:
NAME: POLSBBAIL, BRIAN M.
REGISTRATION NUMBER: 28,462
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Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace(408, "g")
                                                                                                                                                           REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomas, Winston J.
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Feder, John N.
                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.8%;
99.3%;
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222..1268
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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Best Local Similarity
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APPLICANT: Thomas,
APPLICANT: Preder,
APPLICANT: Gnirke,
APPLICANT: Ruddy,
APPLICANT: Ruddy,
APPLICANT: Ruddy,
APPLICANT: Ruddy,
APPLICANT: Ruddy,
APPLICANT: Ruddy,
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LOCATION: replace
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040.6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: /note!= "No. 6025130mal or wild-type (unaformer INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
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LOCATION: 5507..6023

OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d1(G) OTHER INFORMATION: allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) OTHER INFORMATION: allele (SEQ ID NO:41)"
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FEATURE:
NAME/KEY:
LOCATION: 3852.3891
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LOCATION: replace(3878, "a")
OTHER INFORMATION: (phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: (label= 2447)
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASS/FICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SMILCH, WILLIAM M.
REGISTRATION NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATI
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                    E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER. IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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NAME/KEY: -
LOCATION: 140..7319
                                                                                                                                                                                                          CITY: San Francisco
STATE: California
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TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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US-60-487-610-487
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Sequence 1
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1: /cgn2_6/ptcdata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptcdata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptcdata/1/pna/US07_NEW_COMB.seq:*
5: /cgn2_6/ptcdata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptcdata/1/pna/US10_NEW_COMB.seq:*
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8: /cgn2_6/ptcdata/1/pna/US10_NEW_COMB.seq:*
5.1.6
Compugen Ltd.
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US-60-524-882-107
US-60-487-610-19486
PCT-USO3-40978-17631
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US-60-487-610-487
US-60-487-610-487
US-10-741-600-272
US-10-741-600-272
US-60-524-882-114
PCT-US03-40978-266
US-10-741-600-266
US-10-741-600-271
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PCT-US03-40978-261
US-60-524-882-111
PCT-US03-40978-267
US-60-524-882-104
PCT-US03-40978-267
US-60-524-882-109
PCT-US03-40978-267
US-60-524-882-109
PCT-US03-40978-267
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 GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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TITLE OF INVENTION:
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Pred. No. 1.2e-84;
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US-10-741-600-17631

US-60-54-882-9174

US-60-482-9174

US-60-482-9174

US-10-741-600-262

US-10-741-600-262

US-60-524-882-1033

PCT-US03-40978-7447

PCT-US03-40978-7447

PCT-US03-40978-7462

PCT-US03-40978-7480

PCT-US03-40978-7543

PCT-US03-40978-7543

PCT-US03-40978-7549

PCT-US03-40978-7549

US-10-741-600-7363

US-10-741-600-7462

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Best Local Similarity 98.2
Matches 268; Conservative
                                                                                                                                                TYPE: JNA
ORGANISM: Homo sapiens
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Sequence 272, Application US/10741600
| Sequence 272, Application US/10741600
| SEGUENCE AND CONTROL |
| APPLICANT: CREGILL, Michele et al. |
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: MYCOARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
| FILE REFERENCE: CL001499 |
| CURRENT APPLICATION NUMBER: US/10/741,600 |
| CURRENT FILING DATE: 2003-12-22 |
| NUMBER OF SEQ ID NOS: 73997 |
| SOFTWARE: FateSEQ for Windows Version 4.0 |
| SEQ ID NO 272 |
| LENGTH: 746
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GENERAL INFORMATION:
APPLICANT: CARGILL,
APPLICANT: CARGILL,
APPLICANT: APPLICANTON:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERBENCE: CL001494
CURRENT APPLICATION NUMBER: US/60/524,882
CURRENT PILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 46672
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 114
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Pred. No. 2.2e-84;
8; Mismatches 0
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Best Local Similarity 97.1%;
Matches 265; Conservative
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CORGANISM: Homo sapiens
US-10-741-600-272
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US-60-524-882-114
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001499
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongiln
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FASELSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 271; DB 8; Length 2285; Pred. No. 1.3e-84; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
99.3%; Score 271; DB
Best Local Similarity 98.2%; Pred. No. 1.3e
Matches 268; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.88;
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Matches 265; Conservative
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US-60-487-610-487
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LENGTH: 2285
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LENGIH: 746
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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LENGTH: 2009
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TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: PCT/US03/40978
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 266
LENGTH: 2009
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Pred. No. 3.3e-84;
8; Mismatches 0;
                                DB 8;
                              98.8%; Score 269.8; DB 8 97.1%; Pred. No. 2.2e-84; iive 8; Mismatches 0
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Best Local Similarity 97.1%;
Matches 265; Conservative
                                  Query Match
Best Local Similarity 97.1:
Matches 265; Conservative
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERBUCE: CLOOL499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILIAG DATE: 2003-12-22
SUFFMER FILIAG DATE: 2003-12-22
SUFFMER FILE SECTION NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: CARGILL, Michele
APPLICANT: TAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1494
CURRENT APPLICATION NUMBER: US/60/524,882
CURRENT FILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 46672
SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 3.3e-84;
8; Mismatches 0; Indels 0;
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Pred. No. 3.3e-84;
8; Mismatches 0; Indels 0;
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US-60-524-882-108
i Sequence 108, Application US/60524882
i GENERAL INFORMATION:
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97.1%;
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Best Local Similarity 97.1%;
Matches 265; Conservative
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Sequence 113. Application US/60524882
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDITOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/524,882
CURRENT APPLICATION NUMBER: US/60/524,882
CURRENT FILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 46672
SEQ ID NOS: 46672
SEQ ID NO 113
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                                       Indels
Query Match 98.8%; Score 269.8; DB 6; Best Local Similarity 97.1%; Pred. No. 3.5e-84; Matches 265; Conservative 8; Mismatches 0;
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PCT-US03-40978-270
; Sequence 270, Application PC/TUS0340978
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US-60-524-882-113
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US-60-524-882-113
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT PELLING NUMBER: PCT/US03/40978
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 271
LENGTH: 2285
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SAYGAGWGTGGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467
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Matches 265; Conservative
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US-10-741-600-271
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ORGANISM: Homo sapiens
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US-10-741-600-271
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: PCT/US03/40978
CURRENT FILING DAIR: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                        Sequence 111, Application US/60524882

Sequence 111, Application US/60524882

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: TAKOUBOWN: OBNETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION NUMBER: US/60/524,882
CURRENT FILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 46672
SEQ ID NO 111
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Pred. No. 3.5e-84;
8; Mismatches 0;
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                                                                                            241 IGGACTATTATGGAAAATCACAACCAGCAAG 273
                                                                                                                                         528 regacrarraregaaarcacaaccacaecaas 560
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Best Local Similarity 97.1%;
Matches 265; Conservative
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; ORGANISM: Homo sapiens
US-60-524-382-111
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LENGTH: 2440
TYPE: DNA
ORGANISM: Homo sapiens
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US-60-524-882-111
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US-10-741-600-270

US-10-741-600-270

Sequence 270, Application US/10741600

GENERAL INPORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
TITLE OF SEPERAL 2003-12-22

CURRENT PILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFUTARE: PASESEQ for Windows Version 4.0

LENGTH: 2398
                              SENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 3.5e-84;
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: MYCARDIAL INFARCTION, M
FILE REFERENCE: CLOO1499
CURRENT APPLICATION NUMBER: PCT/US03/40978
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 270
LENGTH: 2398
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97.1%; Pred. No. 3.5
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97.1%;
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Best Local Similarity 97.1
Matches 265; Conservative
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Matches 265; Conservative
                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-741-600-270
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                                                          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTTCATGGGTGCCTCAGAGCAGGACCTT
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Query Match 98.8%; Score 269.8; DB 1; Length 2440; Best Local Similarity 97.1%; Pred. No. 3.6e-84; Matches 265; Conservative 8; Mismatches 0; Indels 0;
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4: /cgn2_6/ptodata/1/pna/USO6_COMB.seq:*
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5.1.6
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GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                                                                              - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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273
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Maximum DB seq length: 200000000
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Perfect score:
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Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence 77, Appl Sequence 6940, Ap Sequence 9, Appli Sequence 10, Appl
ID	US-10-138-888-77 US-60-278-232-6940 US-08-834-497-9 US-08-834-497-10
80	4.6 82 13
Query Match Length DB	1440 1440 1440 1440
	100.0 4.99 4.99
Score	273 271.4 271.4 271.4
Result No.	H 01 60 44

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Sequence 6940, Application US/60278232
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
TITLE OF INVENTION: Polynuchisms Identified Thereby
FILE REFERENCE: GX-0011 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCTTGCTGCGTTCACACTCTCTGCACTACTCTTCATGGGTGCCTCAGAGCAGGACCTT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: replace(414, "t")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 8.2e-76;
Matches 273; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                          NAMB: Brian M. Poissant
REGISTRATION UNBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGACTATTATGGAAATCACAACCACAGCAAG 273
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                                                                  FILING DATE: 04 APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
FILING DATE: 02-May-2002
CLASSIFICATION: «UDKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 77:
                                                                                                                                                                                                                                                                          TELEPRONE: (212) 790-9090
TELEPAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1440 base pairs
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222..1268
                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-138-888-77
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                                                                                                                   Sequence 18074, A Sequence 18074, A Sequence 1180, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 18068, A Sequence 18073, A Sequence 18073, A Sequence 2511, Ap Sequence 2579, Ap Sequence 3472, Ap Sequence 3472, Ap Sequence 3472, Ap Sequence 3474, Ap Sequence 3474, Ap Sequence 1581, Ap Sequence 1581, Ap Sequence 1581, Ap Sequence 3474, Ap Sequence 1581, Ap Sequence 3474, Ap Sequence 1581, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Appl
Sequence 12, Appl
Sequence 11, Appl
Sequence 12, Appl
                                                                    Sequence 26715, A
Sequence 27072, A
Sequence 1, Appli
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Sequence 12, Appl
Sequence 11, Appl
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Sequence 41388, .
                                                     Sequence
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
         US-09-497-957-10
US-10-138-888-9
US-10-138-888-9
US-10-170-235-26715
US-10-170-235-26715
US-09-981-606-1
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US-09-920-559-1
US-09-724-676-18068
US-09-724-676-18068
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US-09-724-676-18068
                                                                                                                                                                                                                                                                                                          US-60-452-680-6251

US-60-453-050-3472

US-60-453-050-3472

US-60-455-444-1579

US-60-465-241-1579

US-60-465-241-1579

US-60-465-241-1579

US-60-453-050-3474

US-60-453-050-3474

US-60-453-050-3474

US-60-455-444-1581

US-60-465-241-1581

US-60-465-241-1581

US-60-465-241-1581

US-60-465-241-1581

US-60-467-11

US-09-915-738-1161

US-09-915-738-1161

US-09-915-738-1161

US-09-497-957-11

US-09-497-957-11
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 77, Application US/10138888
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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US-08-834-497-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCTTGCTGCTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADBRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWAREN TO STATEM TO STATEM TO SOFTWAREN TO SOFTWAREN THE PARENTIN BATA:

APPLICATION NUMBER: US/08/034,497
FILING DATE: 04-APR-1997
CLASSIFICATION 435
PRIOR APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/632,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                              99.4%; Score 271.4; DB 82
99.6%; Pred. No. 2.3e-75;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regaciatiaiegaaaicacaaccacaddaad 375
                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 333732.1
CURRENT APPLICATION NUMBER: US/60/278,232
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 12,557
SEQ ID NO 6940
LENGTH: 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08834497
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.6'
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-834-497-9
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288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /phenotype= "normal or wild-type (unaffected)"
/label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 271.4; DB 13;
Pred. No. 2.6e-75;
                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitch Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TEREVETH: 1440 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 TGGACTATTATGGAAAATCACAAACCACAGCAAG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TGGACTATTATGGAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATR:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (unaffected) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= 24d2
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OTHER INFORMATION: /phenoty
OTHER INFORMATION: (unaffect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 222..1268
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: allele
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US-08-834-497-10
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181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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                                                            408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467
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APPLICANT: GALIKE, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: TSUCHIHASHI, SHADITANT
APPLICANT: TSUCHIHASHI, SHADITANT
APPLICANT: TSUCHIHASHI, ZENTA
        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGT
                                                                                                                                                                                                                    241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                      528 regactatraregaaarcacaaccacaacaae 560
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FESTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Poissant, Brian M.
REGISTRATION UNDER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
FILING DATE:
APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
FILING DATE: 23-MAX-1996
FILING DATE: 13-MAX-1996
FILING DATE: 16-APR-1996
FILING DATE: 16-APR-1996
FILING DATE: 16-APR-1996
FILING DATE: 16-APR-1996
ATTORNEY APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY APPLICATION NUMBER: US 08/630,912
ATTORNEY APPLICATION NUMBER: US 08/630,912
ATTORNEY APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                             US-09-497-957-9; Sequence 9, Application US/09497957; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPRANE. 650-493-4935
TELEPRANE. 650-493-5556
TELERS. 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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LOCATION: 222..126
FEATURE:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGCTTGCTGCGTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PX-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-APR-1997
                                                                                                                                                     Hereditary Hemochromatosis Gene
76
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gridke, Andreas
APPLICANT: Gridky, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Worlf, Roger K, TITLE OP INVENTION: Hereditary Hemochromatosis Gen-
NUMBER OF SEGUENCE: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: U4-PK-1397
CLIASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: FILE, Renee A.
REGISTAATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 35,136
REGISTAATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype=
OTHER INFORMATION: /label= 24d1
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TELEFAX: (650) 336-2422
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.63
Matches 272; Conservative
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LOCATION: 222..1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CATGAGTGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 cécriécricacacrererecacracres 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGAGAGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
99.4%; Score 271.4; DB 21; Length 1440;
Best Local Similarity 99.6%; Pred. No. 2.6e-75;
Matches 272; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Feder, John N.
APPLICANT: Galrke, Andreas
APPLICANT: Ruddy, David
BAPLICANT: Tsuchhashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                       /phenotype= "normal or wild-type (unaffected)"
/label= 24d7
                                                                                                                                                                                                                                                                                             /phenotype= "normal or wild-type (unaffected)"
/label= 24d1
                          "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TGGACTATTATGGAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGACTATTATGGAAAATCACAACCACAGCAAG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,957
FILING DATE:
                          /phenotype= "notynaffected) "
/label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09497957
GENERAL INFORMATION:
                     OTHER INFORMATION: /phenotype:
OTHER INFORMATION: (unaffected
OTHER INFORMATION: /label= 24
FEATURE:
NAME/KEY: allele
LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype:
OTHER INFORMATION: /unaffected
OTHER INFORMATION: /label= 24
FEATURE:
                                                                                                                                                                                                                                                NAME/KEY: allele
CCATION: replace(1066, "g")
CTHER INFORMATION: /phenotype
CTHER INFORMATION: (unaffecte)
CTHER INFORMATION: /label= 24
US-09-497-957-9
ION: replace(408, "c")
INFORMATION: /phenotyn
INFORMATION: (unaffect
INFORMATION: /label= 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-497-957-10
    LOCATION:
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61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGCTTGCCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 271.4; DB 21; Length 1440; Pred. No. 2.6e-75; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 regacrarraregaaaarcacaacaacaag 560
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.4%;
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Matches 272; Conservative
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LOCATION: 222..1268
FEATURE:
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121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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                                                                                                                       408 cargagagregecereregagececegaacrecargegrrrecagragaarrreaageceag 467
                                                                                                                                                                       ATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
CORREST APPLICATION NUMBER: US 08/834,497
FILING DATE: 02-May-2002
CLASSIFICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-May-1996
APPLICATION NUMBER: US 08/652,265
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
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TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                     241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-10-138-888-10
is Sequence 10, Application US/10138888
is GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
222..1268
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2711
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type /label= 24d2
                                                                                                                                      COUNTY: NAY JOIK
COMPUTER: NAY JOIK
COMPUTER: BADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: UNMER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/652,655
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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LOCATION: 222..1268
            NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                   CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (unaffected) "
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NAME/KEY: allele

FEATURE

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APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A.MAJORITY OF HUMAN
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CLOO1380
CURRENT APPLICATION NUBBER: US/10/170,235
CURRENT APPLICATION NUBBER: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGTCTTTCCTTGTTTGAAGGTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 GGCTTGCTTCACACTCTGCACTACCTCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 47; Length 2285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1.0 Application US/09981606
GENERAL INFORMATION:
APPLICANT: Rothenberg et al.
TITLE OF INVENTION: Mutations associated with iron disorders;
FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Pred. No. 3.1e-75;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TGGACTATTATGGAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 recherratechanterechechechae 560
                                                                                                      Sequence 27072, Application US/10170235; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.67
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 272, Conservative
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Best Local Similarity
                                       RESULT. 10
US-10-170-235-27072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-170-235-27072
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 27072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2506
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US-09-981-606-1
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GENERAL INFORMATION:
APPLICANT: VERYER, J. Craig
TITLE OF INVERTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CL001380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ_ID NOS: 42514
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LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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99.4%; Score 271.4; DB 47;
Best Local Similarity 99.6%; Pred. No. 2.8e-75;
Matches 272; Conservative 0; Mismatches 1;
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SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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LENGTH: 1724
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                                                                                                                                                                                                                                                        Sequence 18074, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 122181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 18074
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
SUPMER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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Best Local Similarity 99.6
Matches 272; Conservative
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ORGANISM: Homo sapiens
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US-09-724-676A-18074
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US-09-724-676-18074
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307
CURRENT PELICATION NUMBER: US/09/949,016
CURRENT PELING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARE FESTESE FOR WINDOWS VERSION 4.0
SEQ ID NO 1180
LENGTH: 2717
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                                                          Gaps
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Score 271.4; DB 32; Length 2619;
Pred. No. 3.3e-75;
0; Mismatches 1; Indels 0:
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          99.4%;
       Query Match
Best Local Similarity 99.6
Matches 272; Conservative
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Best Local Similarity 99.6
Matches 272; Conservative
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US-09-949-016-1180
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Sequence 64, Application US/09949016

Sequence 64, Application US/09949016

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PEASESEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 2727
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Best Local Similarity 99.64
Matches 272; Conservative
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; ORGANISM: Human
US-09-949-016-64
RESULT 15
US-09-949-016-64
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735 bp mRNA linear PRI 07-MAY-2001
Homo sapiens hemochromatosis splice Variant delE3-7 (HFE) mRNA,
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AR149466 Sequence
AR150664 Homo sapi
Y09800 H. sapiens H
AX701831 Sequence
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AR359892 Homo sapien
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AR359894 Human hered
AR35978 Sequence
AR036573 Sequence
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AR149462 Sequence
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AR149463 Sequence
AR149463 Bomo sapien
AY007544 Binnocero
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AF144242 Homo sapi
AR19233 Sequence
AR275757 Sequence
U60319 Homo sapien
AR117795 Sequence
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I (bases 1 to 735)
Thenie,A., Orhan, Gicquel,I., Fergelot,P., Le Gall,J.Y., David,V. and Mosser,M.
                                                                                                                                                                                                AF115265 Homo sapi
AX407339 Sequence
AR117793 Sequence
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AF149804 Homo sapi
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AR149465 Sequence
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AR275782
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1 cgcttggtgcgttcacactc.....aaaatcacaacacagcaag 273
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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/db_xref="G1:11094313"
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/translation="MGPRAPALLLIMILQTAVLQGRILIRSHSLHYLFWGASEQDLGI
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WTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQVLQDTIYSSEVSSLGIK
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 804)

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                                                                                                         Faculte de Medecine,
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The HFE gene undergoes alternate spliting processes
Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
The HFE gene undergoes alternate splicing processes Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
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Pred. No. 3.9e-76;
0; Mismatches 1;
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                                                          Thenie, R., Orhant, M. and Mosser, J. Direct Submission Submitted (17-DEC-1998) UPR 41 CNRS, Pr. Bernard, Rennes 35043, France Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/chromosome="6"
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Best Local Similarity 99.6%;
Matches 272; Conservative
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/gene="HFE"
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/trānslation="MGPRARPALALLMALQTAVLQGRLLRSHSLHYLEMGASEQDLGL
SLFBALGAYUDDQLFVPYDHESRRVERTPWYGSRISSQWMLQLSQSLKGWDHMFTVDF
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WITLAVPPBEEGRYTCQVSHPGLDQPLIVIWEPSPSGTLVIGVIRGIAVFVVILFIGI
LFILIKRRQGSRGMHYVLARER"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE 99180629
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Homo sapiens hemochromatosis splice variant della
complete cds.
                                                                  Thenie, A., Orbant, M., Gicquel, I. and Mosser, J. Thenie, A., Orbant, M., Gicquel, I. and Mosser, J. Direct Submission.
Submission (1-MAY-1999) Faculte de Medecine, UP du Pr Leon Bernard, Rennes Cedex 35043, France Location/Qualifiers
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Pred. No. 3.9e-76;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/chromosome="6"
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Rhodes, D.A. and Trowsdale, J.
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Best Local Similarity 99.6%
Matches 272; Conservative C
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Homo sapiens (human)
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                              Rhodes, D.A.

Diffect Submitted (21-JUL-1998) Immunology, University of Cambridge, Tennis Submitted (21-JUL-1998) Immunology, University of Cambridge, Tennis Court Road, Cambridge CB2 1QP, UK

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         /protein_id="AAC62646.1"
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QPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFIILRKRQSSRGAMGHYVLAARE
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oliva, R. and Sanchez, M. Identification of different alternative splicing forms of the HFB
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Homo sapiens mRNA for hemochromatosis protein (HPE gene) splice
variant 3.
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/product="hemochromatosis splice variant dell4E4"
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alternative splicing; hemochromatosis protein; HPE gene.
Homo sapiens (human)
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/chromosome="6"
/map="6p22.1"
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/gene="HFE"
37. .1041
/gene="HFE"
                   (bases 1 to 1045)
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264 c 295 g 264 t
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/note="alternative splicing form wit deletion of complete
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2 (bases 1 to .v..,
Oliva,R.
Direct Submission
Submitted (06-SEP-1999) Oliva R., Faculty of Medicine and Clinic
Submitted (106-SEP-1999) Oliva R., Faculty of Medicine and Clinic
Hospital, Human Genome Research Group, Casanova 143, 08036, SPAIN
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Thenie,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y.,
David,V. and Mosser,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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SYTTLRCRALNYYPQNITMKWIKDKQPWDAKREREPKDVLPNGDGTYQGNITLAVPPGE
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SRGAMGHYTLABRE
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                                                                         2 (bases 1 to 1200)
Thenie, A., Orhant, M. and Mosser, J.
Direct Submission
Submitted (17-DEC-1998) UPR 41 CNRS, Faculte de Medecine,
Pr. Bernard, Remnes 35043, France
Location/Qualifiers
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A soluble beta 2 microglobulin (beta2m)/hfe monochain for
biotechnological and therapeutic applications
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   The HFE gene undergoes alternate splicing proces
Blood Cells Mol. Dis. 26 (2), 155-164 (2000)
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Sequence 1 from Patent W00224929.
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/gene="HFE"
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Best Local Similarity 99.6
Matches 272; Conservative
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TKEWRENKTRARQNRAYLBRDCPAQLDELEGRGVLDQQVPPLVKYTHHYTSSYTT
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                    Ramot University Authority for Applied Research & Industrial
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchinhashi,Z. and Wolff,R.K.
Hereditary henchromatosis gene products
Patent: US 6140305-A 9 31-OCT-2000;
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                                                                                         'organism="synthetic construct"
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/note="unnamed protein product"
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/transl_table=11
/protein_id="CAD35231.1"
/db_xref="G1:21440047"
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/note="synthetic"
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Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Thomas, W.J., and Wolff, R.K.
Tsuchihashi, Z. and Wolff, R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 9 08-MAY-2001;
Location/Qualifiers
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 10 08-MAX-2001;
Location/Qualifiers
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Hereditary hemochromatosis gene products
Patent: US 6140305-A 10 31-OCT-2000;
Location/Qualifiers
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PAT 20-APR-2002
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                               250 generintecineringaageninggeenacendaahdaccadenericendinenanan 309
                                                                CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                              310 cargagagregecerergagececegaacrecargagrirecagragaarrreaagecag 369
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Rothenberg, B.E., Sawada-Hirai, R. and Barton, J.C. Mutations associated with iron disorders
Patent: US 635425-A 112-WAR-2002;
Location/Qualifiers
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Pred. No. 4.2e-76;
0; Mismatches 1;
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Sequence 1 from patent US 6355425.
AR199238
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/organism="unknown"
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Matches 272; Conservative
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WTIMENHNHSKVPPLVKVTHHYTSSYTTLRCRALNYYPQNITWKWLKDKQPNDAKBFE
WACADPWGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIGVI
SGIAVPVVILPIGILFILLRKRQGSRGAVGHYVLAERE"
A 442 c 458 9 532 C
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/db xref="GI:11094325"
/translation="MGPRARPALLLIMLLQTAVLQGRLLRSHSLHYLFWGASEQDLGL
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Thenie,A., Orhant,M., Gicquel,I. and Mosser,J.
Direct Submission
Submitssion
Submitted (20-APR-1999) Faculte de Medecine, UPR41 CNRS, 2 Avenue
du Pr. Leon Bernard, Rennes Cedex 35043, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Dutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 1885)
Thenie,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y., David,V. and Mosser,J.

The HFE gene undergoes alternate splicing processes
Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
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                                      GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
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                                                                                CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG
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/product="hemochromatosis splice variant delE3"
                                                                                                                                                                                                                                                                                                                                    AF144242 120 1885 bp mRNA linear PRI Homo sapiens hemochromatosis splice variant delE3 mRNA,
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Pred. No. 4.1e-76;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                         TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p22"
                                                                                                                                                                                                                                                                                                                                                                                                    AF144242.1 GI:11094324
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124. .894
/gene="HFE"
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Matches 272; Conservative
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HOMO Sapiens haemochromatosis protein (HLA-H) mRNA, complete cds.
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1 (bases 1 to 2727)

Feder, J.N., Gnirke, A., Thomas, W., Tsuchihashi, Z., Ruddy, D.A., Basava, A., Dormishian, F., Domingo, R., Ellis, M.C., Fullan, A., Hinton, L.M., Jones, N.L., Kimmel, B.E., Kronmal, G.S., Lauer, P., Lee, V.K., Loeb, D.B., Mapa, F., McClelland, E., Meyer, N.C., Mintier, G.A., Moeller, N., Moore, T., Morkang, E., Prass, C.E., Ountaana, L., Stranes, S.M., Schatzman, R.C., Brunke, K.J., Drayna, D.T., Risch, N.J., Bacon, B.R. and Wolff, R.K.

A novel MHC class I-like gene is mutated in patients with
                                                                                                                                                                                                                                                                                09
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Submitted (10-JUN-1996) Mercator Genetics, 4040 Campbell Ave., Menlo Park, CA 94025, UGA
                                                                                                                                                                                                                                                                              1 GGCTTGCTGCGTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                          Length 2506;
                                                                                                                                                                                                                                    Indels
Rothenberg, B.E., Sawada-Hirai, R. and Barton, J.C. Mutations associated with iron disorders Patent: US 650942-A 1 21-JAN-2003; Location/Qualifiers
                                                                                                                                                                                        Score 271.4; DB 6;
Pred. No. 4.2e-76;
0; Mismatches 1;
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Nat. Genet. 13 (4), 399-408 (1996)
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Location/Qualifiers
                                                                                                         /organism="unknown"
                                                                                                                               596 g
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Best Local Similarity 99.6%;
Matches 272; Conservative
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                          TITLE
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AUTHORS
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HSU60319
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SVTTLRCRALMYYPQNITMKNLKDKQPNDAKEFEPKDYLENGEGTYGGNITLAVPPGE
SQRYTCQVBHPGLLDPLIVINBPSPSGTLVIGVISGIAVFVVILFIGILFIILRKRQG
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WTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLBFCFDTLDWRAAEP
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochronatosis gene products
Patent: US 6140305-A 11 31-OCT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.4%; Score 271.4; DB 9; Length 2727; Best Local Similarity 99.6%; Pred. No. 4.2e-76; Matches 272; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                               /codon_start=1
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                                                                                         note="synonym: HFE"
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chromosome="6"
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              /map="6p21.3"
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181 AIGTGGCTGCAGCTGAGTCCAGAGTCTGAAAGGGTGGGATCACAGTTTCACTGTTGACTTC 240
288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347
                        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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Search completed: February 11, 2004, 19:15:40 Job time : 1636.78 secs

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AA177236 mu89505.r

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AU138140 AU138140
CB960984 AGENCOURT
ALS50540 ALS50540
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K-EST0027329 S9SNU601 Homo sapiens cDNA clone S9SNU601-12-G03 5',
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Kim, M.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kim YS
Genome Research Center
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
S2 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungsmail.kribb.re.kr
Plate: 12 row: G column: 03
High quality sequence stop: 544.
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Unpublished
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AV65852
AL547869
CB154892
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KEYWORDS
SOURCE
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JOURNAL
COMMENT
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AUTHORS
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BM751283
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                                                                                                                                                  1 cgcttgctgcgttcacactc.....aaaatcacaaccacagcaag 273
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AU279987
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                                                            - nucleic search, using sw model
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em_estpl: *
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gb_estl: *
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Perfect score:
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Minimum DB 8 Maximum DB 8

Database

Result No.

Searched:

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AU132916 AU132916

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                              Contact: Takao Isogai
Genomics Laboratory
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Redifferentiation of dedifferentiated chondrosytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with an expression profiling by large-scale cDNA analysis
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases, 1 to 560)
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Pred. No. 6.3e-75;
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                                                 organism="Homo sapiens"
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Email: genomics@hri.co.jp
HRI human CDNA Project, Sugiyama,T.; Wakamatsu,A.; Irie,R.; Umezawa
HRI human CDNA Project, Sugiyama,T.; Wakamatsu,A.; Irie,R.; Umezawa
,A.; Fukuma,M.; Kuakari,S.; Hata,J.; Ishii,S.; Yamamoto,J.; Isono
,Y.; Saito,K.; Nakamura,Y.; Masuho,Y.; Nagai,K.; Isogai,T.
HRI human CDNA project; CDNA library construction & 5'-end one
pass sequencing: Helix Research Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-866-44770
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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
151-1 81-438-52-3975
Fax: 81-438-52-3986
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Pred. No. 6.4e-75;
0; Mismatches 1
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21C Frontier Korean EST Project 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell type="chondrocytes"
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143 c 168 g 124
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Parent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J. Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush, J. and Keele, J.W.
                                                                                                                         Email: asimpsonolludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be set in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&tL2=PM4-BT0209-151200-003-£07&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence start: 17
High quality sequence stop: 384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly Mamm. Genome 13 (8), 475-478 (2002)
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 ACCAGCTGTTCGTGTTCTATGATCATGAGTGTCGCCGTGTGGAGCCCCCGAACTCCATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 TGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTTGAAGCTTTGGGGCTACGTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 ATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACCAGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Length 384;
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 222.4; DB 10
Pred. No. 1.8e-59;
0; Mismatches 1
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112 c 87 g 93 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.5%;
99.2%;
                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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PM4-ET0209-151200-003-f07 ET0209 Homo sapiens cDNA, mRNA sequence.
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1 (bases 1 to 384)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bais,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                     /lab host="Top10F'"
/clone lib="L17NG70205n1"
/clone lib="L17NG70205n1"
/note="Yogan: Liver; Vector: pT7T3-Pac; Site_1: BcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
culture."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIGIGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 GGTCTTTCCTTGTTTGAAGCTTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
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0
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                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L17N670205n1-27-D07"
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Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 t
          Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: D column: 07
                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                     High quality sequence stop: 535.
Location/Qualifiers
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EST 18-OCT-2000

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
vv.990904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
POR PRIMERS
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mu89b05.rl Soares mouse lymph node NbMLN Mus musculus cDNA clone IMAGE:652689 5' similar to TR:G940354 G940354 CLASS I HISTOCOMPATIBILITY ANTIGEN-LIKE PROTEIN: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 464)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 caccadadrececerdecadadeerececececeredererecegraadeeerecedaa 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 CTGTGGCTGCAGCTAAGCCAGAGCCTGAAAGGGTGGGATCACATGTTCACCGTGGACTTC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGGGGGGGCACACACCCTGCTCTTCATGGGCGCCTCGAAGCCAGATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                          /lab hode: "DH10B"
/clone lib="MARC 2PIG"
/clone lib="WARC 2PIG"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Si
/ibrary made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta.'
a 180 c 164 g 98 t
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.0%; Score 180.2; DB 12; Length 550; dlarity 78.8%; Pred. No. 5.2e-46; Conservative 0; Mismatches 58; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGACCATCATGGACAACCACAACTACAGCAAG 414
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Unpublished
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 100 row: C column: 24
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. .550
/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                       scrofa"
                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
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402 762 4390
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/db__type="mRNA"
/db__type="mRNA"
/tisue_type="pooled"
/lab_host="MHOB"
/clone_lib="MARC 2PIG"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, ovary,
endomecrium, hypothalamus, pituitary, and placenta."
                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 550)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAGCGCCGCCCACACACCCCTGCTCTTCATGGGCGCCTCGGAGCCAGATCTC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,J. and Keele,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.0%; Score 180.2; DB 10; Length 523; 78.8%; Pred. No. 5e-46; ive 0; Mismatches 58; Indels 0;
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364041 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BI339179
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 TGGACCATCATGGACAACCACAACTACAGCAAG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mamm. Genome 13 (8), 475-478 (2002)
                                                                                                                                                                                                                                                                                                       organism="Sus scrofa"
                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCATCACGACG
Plate: 48 row: E column: 9
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 215; Conservative
Tel: 402 762 4366
Fax: 402 762 4390
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Sus scrofa
                                                                                                                                                                                                                                                                                   1. .523
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BI339179
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara, Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii, Y., Yolto,M., Kawali,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numaaski,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Ashaira,S., Tanaka,T., Tanaku,T., Tayai,T., Watahiki,A., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-resegescriken.go.jp,

Carninci,P., Genome-gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

Mr. Komo,H., Okazaki,Y., Muramateui,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA ibbaries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,M., Ohara,E.,

Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

Hayashizaki,Y.
                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 CTGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 certretrreagecraegecrarcresareaccaecretricrerecraeareage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CTGCGTTCACACTCTGCACTACCTCTTCATGGGTGCCTCCAGAGCAGGACCTTGGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="G370002P09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
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Matches 210;
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           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB851691 RIKEN full-length enriched, B16 F10Y cells Mus musculus cDNA clone G370002P09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares mouse lymph node NbMLN"
hote="Organ: lymph node; Vector: pT713D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not 1: Site 2: Eco RI;
let strand cDNA was primed with a Not I - oligo(dT) primer
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                 Email: moueeest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:398537
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 CTGCATCTGAGGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 CCTTTGTTTGAGGCTAGGGCTATGTGGATGACCAGCTCTTTGTGTCTACAATCATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 AGTOGOCGIGOTGAGOCCOAGGGOCCOGIGGATOTIGGAGCAAACCICAAGCCAGCIGIGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CTGCGTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 TGTCGCCGTGTGGAGCCCCGGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG
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  Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="lymph node"
/dev stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 ATTAIGGAAAAICACAACCACAGCAAG 273
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                                                                                                                                                                                                                                                                                                                                            'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                'db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:652689"
                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local S:
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DEFINITION

RESULT 9 BE994943

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

JOURNAL MEDLINE PUBMED

AUTHORS TITLE

REFERENCE

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Mus musculus

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mus musculus

Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(b. (b. 2014)

Cokazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,

Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,

Quackenbush, J., Schriml, L.M., Ranapin, A., Matsuda, H., Batalov, S.,

Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, J.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., R., Gough, J., Gramenod, S., Hirokawa, N., Jackson, I.J.,

Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,

King, B. L., Konagaya, A., Kurockhin, I.V., Lee, Y., Lenhard, B., Lyons

P. A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki,

H., Nagashima, T., Numata, K., Oskido, T., Pavan, W.J., Percea, G.,

Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring

A. Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale

R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,

M., Shada, M., Sandelin, A., Schneder, C., Semple, C., Wang, Y.,

M., Shazume, N., Sato, K., Shiraki, T., Wahlestedt, C., Wang, Y.,

M., Sakazume, N., Sato, K., Shiraki, T., Wahlestedt, C., Wang, Y.,

Arakawa, T., Fukuda, S., Harozane-Kishikawa, T., Konno, H., Nakawura,

M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Sawai, D., Shibata

M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Sawai, D., Shibata

M., Sakazume, M., Sato, K., Shiraki, Y., Waki, K., Sawai, D., Shibata

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M., Sakazume, Y., Wang, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata

M., Sakazume, M., Sato, K., Shiraka, W., Yangi, Sato, D., Shibata, M., Sato, M., Sato, M., Sakai, M., Sakai, M., Sato, M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-rese@gac.riken.go.jp,
URL:http://genome.gac.riken.go.jp/
URL:http://genome.gac.riken.go.jp/
Acadehi,U., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imoteni,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
                                                         119 CCTTTGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG 178
       TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
                                                                                                                                                                                                                          179 AGTOGOCÓTIGOTGAGOCOCAGGOCOCOGTIGATOTTGGAGOAAACOTOAAGOCAGOTIGTIGG 238
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BY747346 RIKEN full-length enriched, 2 days neonate thymus thymic cells (NoD) Mus musculus CDNA clone B430034J19 5', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                     127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                             247 ATTATGGAAAATCACAACCACAGCAAG 273
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Mus musculus
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Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12466851
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/lab host="mildle (Life Technologies)"
/lab host="mildle (Life Technologies)"
/clone lib="NIH BMAP Ret4 52"
/note="Voctor: pTyT35" Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Ecc RI; The
NIH BMAP Ret4 52 library is a subtracted library.
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enail: mESTGemail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP CDNA
clones from RESEARCH GRETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP CDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The tissue for this library was contributed by Dr. Xin-Yuan Fu,
Yale University School of Medicine The following repetitive
elements were found in this CDNA sequence: 1-31, >(CAG
                                                                                                                                                                                                                          BE994943 489 bp mRNA linear EST 29-APR-2002 UL-M-CGOp-bik-d-03-0-UI.81 NIH BMAP_Ret4 S2 Mus musculus cDNA clone UI-M-CGOp-bik-d-03-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

    (bases 1 to 489)

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Normalization and subtraction: two approaches to facilitate gene
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64.4%; Score 175.8; DB 10; Length 489;
Best Local Similarity 78.7%; Pred. No. 1.2e-44;
Matches 210; Conservative 0; Mismatches 57; Indels 0;
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
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/strain="C57BL/6J"
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Fax: 301 443 9890
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FEATURES

59 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 118

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HTC; CAP trapper.
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Human Genome Sequences Mamu. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust (MRC building Addenbrookes Hospital Cambridge) whose
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,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazune,N., Sano,H.,
Sasaki,D., Sato,K., Shibata, K., Shibata, T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with
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thymus_thymic_cells (NOD)"
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Please visit our web site (http://genome.gsc.riken.go.jp)
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64.4%; Score 175.8; DB 1.
Best Local Similarity 78.7%; Pred. No. 1.5e-44;
Matches 210; Conservative 0; Mismatches 57
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/strain="NOD"
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                                                                                                               Submission
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AK088986
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HTC 05-DEC-2002

AK088986 1719 bp mRNA linear HTC 05-I Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430034119 product:hemochromatosis, full insert sequence.

AK088986

ACCESSION

DEFINITION

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Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,T., Isara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Saito,T., Gojobori,T., Bono,H., Kasukawa,T., Saatto,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischman,W., Gasterland,T., Gissi,C., King,B., Kochiwa,H., Ruehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Kuchi,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Andelli,P., Lewis,S., Matsuo,Y., Nikaido,I., Pusole,G., Tomita,M., Baldarelli,R., Barsh,G., Sakai,K., Okido,T., Puruo,M., Anno,H., Baldarelli,R., Barsh,G., Bakai,K., Okido,T., Puruo,M., Anno,H., Baldarelli,R., Barsh,G., Bakai,K., Okido,T., Puruo,M., Bult,C., Hoffmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Hoffmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ring,B., K., Kadiald,M., Rodriguez, I., Sakamoco,N., Sasaki,H., Sobida,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L., Whynshw.Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
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Analysis of the mouse transcriptome based on functional annotation 6 f60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1719)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                        Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Komo, H., Adachi, J., Fukuda, S. Arakawa, M., Ishi, K., Kiyosawa, H., Komoo, S., Yamanaka, I., Saito, T., Saito, T., Gojobori, T., Bono, H., Kasukawa, T., Satto, R., Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kochiwa, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuo, M., Anno, H., Baldarelli, R., Barshio, T., Sakai, K., Okido, T., Furuo, M., Anno, H., Fletcher, C., Fullita, M., Gariboldi, M. Gustincio, S., Hill, D., Hofman, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, T., Sakanoco, N., Sasaki, H., Schobach, C., Seya, T., Sakanoco, N., Sasaki, H., Toyo-oka, K., Wang, K.H., Weltz, C., Willming, L., Walttaker, C., Wilming, L., Walti, Weltz, C., Wilming, L., Walti, Walti, K., Kawaji, H., Kohtsuki, S., M., Walti, L., Walti, K., Wawaji, H., Kohtsuki, S.
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                                                                                                                                                                                                                                                                                                                                          HTC 05-DEC-2002
                               358 CTGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 417
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                   AK009581 1723 bp mRNA linear HTC 05-DEC-2
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310032M04 product:hemochromatosis, full insert
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                           247 ATTATGGAAATCACAACCACAGCAAG 273
                                                                                                                                                                                    418 Arcardegeaacraraaccacagraag 444
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AK009581.1 GI:12844462
HTC: CAP trapper.
Mus musculus (house mouse)
Mus musculus
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LGLPLFBARGYVDDQLFVSYNHESRRAEPRAPWILEQTSSQLWIHLSQSLKGWDYMFI
VDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWRYGYDGQDHLEFC
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TLVKVTRHWASTGTSLRCQALDFFPQNITWRWLKDNQPLDAKDVNPEKVLPNGDETYQ
GWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVGI
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'clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (STERN), Laboratory for Genome Exploration Research (COUD, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Sangawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL.http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
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                                      Takaku-Akahira,S.,
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(MGD|MGI:109191)
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Takeda,Y., lagami,M., Tagawa,A., Takahashi,F., Takaku-Ai
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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Pred. No. 2.2e-44;
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37. .1173
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/db_xref="GI:26354116"
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/clone="E430034J19"
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/strain="NOD"
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78.7%;
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BG747345.1 GI:14057998
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78.7%;
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                                       Query Match
Best Local Similarity 78.7
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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TITLE
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IVDFWTIMGRYNHSKYTKLGYVSEAHILQVVLGCEVHEDNSTSGFWRYGYDGQDHLEF
CPKTLNWSAAEPGAWATKVEWDEHKI RAKQNHDYLEKDCPEQLKRLLELGGQV
PTLVKVTRHASJGTSLRCQALDFPDNITWWLKDNQPLDAKDVNDEKVLPNGDETY
QGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVG
                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="tongue"
/clone lib="RIKGN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MSLSAGLPVRPLLLLLLLWSVAPQALPPRSHSLRYLFMGASEP
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phases I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
                                                                                                                 Adachi, J. Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Fukuo, M., Hanaqaki, T., Hara, A., Hayatan, M., Hiramoto, K., Hiraoka, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Izawa, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Yoshino, M., Muzamatsu, M. and Hayashizaki, Y. Tanaka, T., Yoshino, M., Muzamatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="unnamed protein product; hemochromatosis | MGD | MGI:109191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="CS7BL/6J"
/db.xref="FANTON DB:2310032M04"
/db_xref="MGI:1905246"
/db_xref="taxon:10090"
/clone="2310032M04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407
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db_xref="GI:12844463"
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1. .1723
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                                                                              Nature 420, 563-573 (2002)
6 (bases 1 to 1723)
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/db zref="raxon:9606"
/dloze="mkNA"
/db zref="taxon:9606"
/clone="IMAGE:4857941"
/tlssue type="adenocarcinoma cell line"
/tlssue to the tollow cell line cel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 CIGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 422
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: ArCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Linn at:
http://image.linl.gov
Plate: LicMill row: d column: 06
High quality sequence stop: 792.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                 Gaps
                                                                                                                            0;
           DB 11; Length 1723;
                                                                                                                      57; Indels.
Score 175.8; DB 1
Pred. No. 2.3e-44;
0; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 ATTATGGAAAATCACAACCACAGCAAG 273
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/organism="Homo sapiens"
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Gaps

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Numaculus, Eutheria; Rodentia; Sciurognath; Muridae; Mutinae; Muscatulus, Bukaryota; Merazoa; Chordata; Sciurognathi; Muridae; Mutinae; Muscatulus; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscazki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagik, T.; Malazelii, R.; Hill, D. P.; Bult, C.; Hume, D.A.; Colobori, T.; Balazelii, R.; Hill, D. P.; Bult, C.; Hume, D.A.; Dalazelii, R.; Hill, D. P.; Bult, C.; Hume, D.A.; Deckenbush, J.; Schrimi, L.; Marapin, A.; Matsuda, H.; Batalao, S.; Beisel, K.W.; Blake, J.A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L.; Cousins, S.; Dalla, E.; Dragani, T.A.; Fletcher, C.F.; Forrest, A.; Farzer, K.S.; Gassterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gugh, J.; Girmmond, S.; Gugtin, C.C.; Lev, M.; Jackson, I.J.; Jackson, J.; King, B.L.; Konagaya, A.; Kurochkin, I.V.; Lee, Y.; Leharad, B.; Lyons, P.B.; Maglott, D.R.; Marchionni, L.; McKenzie, L.; Miki, H.; Namata, K.; Okido, T.; Pevan, W. J.; Pertea, G.; Pertovsky, N.; Piliad, B.; Redid, J.; Reid, J.; Reid, J.; Rangolet, G.; Petrovsky, N.; Piliad, R.; Pottius, J.J.; Teshd, J.; Rangolet, S.; Ravasi, T.; Reed, D.J.; Reid, J.; Reid, J.; Rangolet, S.; Ravasi, R.; Magner, L.; Wanlestedt, C.; Semple, C.A.; Schoule, R.; Bultana, R.; Takenaka, Y.; Taylor, M.; Yang, I.; Yang, L.; Yang, L.; Wang, Y.; Mang, Y.; Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                     127 TGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY745026 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830071K08 5', mRNA sequence.
                                                                                                                                                                                                                                                   7 CIGCGIICACACICICIGCACIACCICIICAIGGGIGCCICAGAGCAGGACCIIGGICII
                                                                                                               Score 174.8; DB 10; Length 392;
Pred. No. 2.3e-44;
0; Mismatches 58; Indels 0;
                              93
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TAG_SEQ=None found"
107 c 115 g
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                                                                                                                         64.0%;
78.3%;
                                                                                                                  Query Match
Best Local Similarity 78.33
Matches 209; Conservative
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/clone="VI-M-CGOp-bgp-a-01-0-VI"
/lab host="BH10B (Life Technologies)"
/clone lib="WIH BNAP Ret4 S2"
/note="Vector: pT7T3D-pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
Not BNAP Ret4 S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.ulowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Xale
University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mESTGemail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soarse Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soarse
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The following repetitive elements were found in this cDNA sequence:
1-31, >(CAG)TH$Simple_repeat
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF465475 1392 bp mRNA linear EST 04-DEC-2000 UI-M-CG0p-bqp-a-01-0-UI.s1 NIH BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CG0p-bqp-a-01-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                        157 GTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGG 216
                                                                                                                                                                                                                                                                                                                          61 GTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGG 120
                                                                                                                                                           97 GACCAGCTGTTCGTGTTCTATGATCATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I boasa; I to agas; Mus. Bonaldo, M.P., Lennon, G. and Soares, M.B.
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                              .,
                           Query Match

64.2%; Score 175.4; DB 10; Length 819;
Best Local Similarity 99.4%; Pred. No. 2.1e-44;
Matches 176; Conservative 0; Mismatches 1; Indels 0;
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EST 17-DEC-2002

09981606-la copy 67 339.rst

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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Email: 91-45-503-9216
Email: genome-rese@ggc.riken.go.jp,
URL:http://genome-ggc.riken.go.jp,
URL:http://genome-ggc.riken.go.jp,
IRI:http://genome-ggc.riken.go.jp,
IRI:http://genome-ggc.ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center, and Genome Science Laboratory in RIKEN.
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Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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/tissue type="bone marrow"
/cell type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow
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78.3%; Pred. No. 2.9e-44;
.ive 0; Mismatches 58; Indels
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Contact: Yoshihide Hayashizaki
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Search completed: February 11, 2004, 19:57:33 Job time : 1560.87 secs

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February 11, 2004, 15:39:51; Search time 200.887 Seconds (without alignments) 3668.467 Million cell updates/sec
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| SIDS1/gggdata/geneseque emb1/NA1981.DAT:
| SIDS1/gggdata/geneseque emb1/NA1981.DAT:
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| SIDS1/gcgdata/geneseq_geneseq_n-emb1/NA2099.DAT:*
| SIDS1/gcgdata/geneseq_geneseq_n-emb1/NA2000.DAT:*
| SIDS1/gcgdata/geneseq_geneseq_n-emb1/NA2001A.DAT:*
| SIDS1/gcgdata/geneseq_geneseq_n-emb1/NA2001A.DAT:*
| SIDS1/gcgdata/geneseq_geneseq_n-emb1/NA2001B.DAT:*
| SIDS1/gcgdata/geneseq_geneseq_n-emb1/NA2002.DAT:*
| SIDS1/gcgdata/geneseq_geneseq_n-emb1/NA2003.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          - nucleic search, using sw model
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length: 2000000000
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	Description	DNA encoding beta	Hereditary haemoch	Human hereditary h	Human hereditary h	cDNA sequence enco	Haemochromatosis g	Human hereditary h	Human hereditary h
		ABK49917	AAT96691	AC68429	AAC68430	AA96769	AV23525	AC68431	AC68432
	G.	24 A	. A						22 A
	DB	:	ã	22	22	21	19	22	
	Length	1317	1440	1440	1440	2506	2727	1440	1440
% Query	Match Length DB ID	99.4	99.4	99.4	99.4	99.4	99.4	98.8	98.8
	Score	271.4	271.4	271.4	271.4	271.4	271.4	269.8	269.8
Result	No.	-	7	m	4	5	9	7	8

Human colon specif	itary	Human hereditary h	Human hereditary h	Genomic DNA of a h	Hereditary haemoch	r)	Human hereditary h	hereditary	Human polynucleoti	Human HLA-H exon 2	Human HLA-H exon 2	Oligonucleotide Dl	Oligonucleotide D1	Oligonucleotide D1	Oligonucleotide D1	Human polynucleoti	Human secreted pro	Human HFE peptide	Bovine mammary tis	DNA fragment with	Probe used for gen	ding	class I anti	MHC class I antige	lass		Nucleic acid seque	Human polymucleoti	Human polynucleoti	Human MHC class I	YF-VI DNA sequence	Chicken MHc class	Human secreted pro	Sequence surroundi	Human cDNA differe	cDNA encoding chic	
ABV93934	σ,	AAC68425	AAC68426	AAA96794		AAV57903		AAC68428	AA163897	AAH02413	AAH02414	AAF58231	AAF58232	AAF58246	AAF58247	AA163896	39	AAA62424	AAF92308	AAH78015	AAA12669	AAA48668	AAX89246	AAX89245	AAV34456	AAD29183	26	AA163914	AA 163816	ABZ74995		Ф	AAC08552		57	AAA48669	
25	18	22	22	21	19	19	22	22	22	22	22	22	22	22	22	22	21	21	22	22	21	21	20	20	19	24	20	22	22	25	24	24	21	22	24	21	
5982	10825	10825	10825	12146	ന	237326	10825	10825	596	100	100	96	97	75	75	575	491	51	430	47	45	1112	1032	1032	2380	264	3324	448	1001	12930	261	261	313	40	148834	23	
											35.5					19.9			17.7	16.6	16.5	16.0	16.0		15.2						14.5			14.1	14.1	13.8	
261.4	61	61	261.4	61	61	61.	59.	59.	S		v	4.	ά.	8	è.	54.4	m	51	•	45.4	45	•	43.6	4	41.6	40.6	ö	40	40	40	6	6	8	8	38.4	7.	
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ALIGNMENTS

RESULT 2

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The invention relates to a soluble polypeptide (I) of beta 2

microglobulin (beta2m)/HFE monochain comprising human beta2m (or its

analogue or active fragment). linked to alphal-alphaad domains of human

CHEE (a central regulator of iron absorption; undefined), or its analogue

or active fragment, by a flexible linker peptide, or a functional

Gerivative or all of (I). (I) is useful for reducing intracellular iron

absorption in patients having hereditary hemochromatosis, transfelusions,

thalassaemias, haemolytic anaemia or chronic infections, and for

delivering a therapeutic to ceals that over-express transferrin receptor

(TfR) which are preferably lymphocytes or leukocytes, across the blood-

comparison (I) is further useful for treating brain tumour. (I)

is also useful for treating oxidative stress disorders resulting in

ctissue damage e.g. vascular diseases, inflammation, atherosclerosis,

lung injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful

cc as a platform for drug delivery of therapeutic use for cancer,

cutoimmune diseases and inflammatory conditions. The monochain manifests

specific characteristics advantageous for drug delivery systems. It is a

soluble, stable and fully conformed protein. It binds specifically to

transferrin receptor. If is continuously internalised by the target cells, thus

colling efficient drug delivery. It dissociates from the recepton,

cells, minimising side effects. It negatively regulates iron absorption,

cells, minimising aide effects. It negatively regulates iron absorption,

cells, minimising side effects. It negatively regulates iron absorption,

cells, minimising side effects. It negatively regulates iron and delivery of

drugs via monochain is expected to overcome drug-resistance since it is a

coding sequence of beta2m/HFE monochain sequence represents the
                                                                                                                                                                                                                                                  Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by
                                                UNIV RAMOT APPLIED RES & IND DEV LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding sequence of beta2m/HFE monochain.
                                                                                                                          Laham N;
                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 2; 77pp; English.
                                                                                                                          Rotem-Yehudar R,
22-SEP-2000; 2000US-234843P.
                                                                                                                                                                        WPI; 2002-383192/41.
P-PSDB; AAU80035.
                                                                      MCINNIS P.
                                                                                                                                                                                                                                                                                                                                   a linker peptide
                                                                                                                       Ehrlich R,
                                                                      (MCIN/)
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Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;

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                                                                                                                                                       463 GGTCTTTCCTTGTTTGAAGCTTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
                                                                                                                                                                                     CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG
                                                                                                                                                                                                                                                ATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC
                                                                                          403 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                          GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
                                                                                                                                                                                                               cargadactogocororodadocococarocorrecagnadarrroadocad
                                                            CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                               Gaps
Score 271.4; DB 24; Length 1317; Pred. No. 2.7e-79; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                              TGGACTATTATGGAAAATCACAAACCACAGGAAG 675
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 99.4%;
                               Conservative
              Local Similarity
                            272;
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 Query Match
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Hereditary haemochromatosis gene and variants - useful for diagnosis and treatment of hereditary haemochromatosis disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmid-based cDNA library following identification of the HH locus in the HLA region of chromosome 6. A single mutation (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a Cys to Tyr substitution in the encoded protein (see AAW36499) at a Cys to Tyr substitution in the encoded protein (see AAW36499) at a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Critical disulphide bridge important for secondary structure. The following are claimed: a 10825 bp genomic DNA sequence (I) (see AAT96690), the 1437 bp cDNA sequence (Ia) and their 24d1, 24d2 and 24d7 variants; a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method mutation; an animal model for the HH disease; metal chelation
                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= i
/note= "G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
                                                                                                                                                                                                                                                                                  /*tag= g
/note= "C to G substitution (24d2 mutation)
                                                                                                                                                                                                                                                                                                                  results in His to Asp substitution"
                                                                                                                                                                                                                                                                                                                                                               "A to T substitution (24d7 variant) results in Ser to Cys substitution"
                                                                                                                                     Hereditary haemochromatosis; metal toxicity; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomas WJ;
                                                                                                        Hereditary haemochromatosis gene cDNA clone.
                                                                                                                                                     gene therapy; prenatal screening; human; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruddy D,
                                                                                                                                                                                                                 Location/Qualifiers
222.1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gnirke A,
             AAT96691 standard; cDNA; 1440 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MERC-) MERCATOR GENETICS INC.
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96US-0630912.
96US-0632673.
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                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drayna DT, Feder JN, Gn
Isuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                 /*tag=
/note=
                                                                                                                                                                                                                                                    *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW36499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-1997;
                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9738137-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-1996;
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16-APR-1996;
                                                                         14-APR-1998
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                                                                                                                                                                                                                                                                                                                                  variation
                                         AAT96691;
                                                                                                                                                                                                                                                                 mutation
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AAT9669
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09981606-1a_copy_67_339.rng

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agents, T-cell differentiation factors and therapeutic agents for
the mitigation of injury due to exidative process in vivo or
mitigation of iron overload; a method for screening potential
therapeutic agents for activity in connection with HH disease; an
antisense oligonucleotide directed against a transcriptional
product of a nucleic acid sequence as above; and oligonucleotides
or pairs of oligonucleotides covering a range of nucleotides from
(1), (1a) or their variants, useful for detecting a polymorphism in
the HH gene. The invention also relates to methods for screening
of for HH homozygotes, to HH diagnosis, prenatal screening and
diagnosis, and therapies of HH disease, including gene therapy,
protein- and antibody-based therapeutics, and small molecule
therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGAGTGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG
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                                                                                                                                                                                                                                                                                                                                                                               288 GGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                              348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
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                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                             Score 271.4; DB 18; Length 1440;
Pred. No. 2.8e-79;
0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                               Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 TGGACTATTATGGAAATCACAACCACAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human hereditary hemochromatosis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC68429 standard; DNA; 1440 BP
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96US-0632673.
96US-0652265.
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                                                                                                                                                                                                                                                                                                al Similarity 99.6
272; Conservative
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                                                                                           The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
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                                                                                                                                                                                                                                       99.4%; Score 271.4; DB 22; Length 1440; 99.6%; Pred. No. 2.8e-79; ive 0; Mismatches 1; Indels 0;
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                                                                 Disclosure; Fig 4; 108pp; English
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96US-0632673.
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16-APR-1996;
23-MAY-1996;
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187
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                                                         The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequence encoding a histocompatibility iron loading (HFE) protein.
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for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
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S65C"
                                                                                                                                                         DB 22; Length 1440;
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H63D"
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                                                                                                                                    Seguence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;
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"if this base is mutated to T,
protein contains the mutation
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Pred. No. 2.8e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human histocompatibility iron loading (HFE) protein. The HFE gene is a major histocompatibility (MHC) mon-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the aisorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number U60319). The presence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic
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                          "if this base is mutated to C, then the protein contains the mutation I105T, which is associated with an iron overload disorder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sawada-Hirai R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BILL-) BILLUPS-ROTHENBERG INC
                                                                                                                                                                                                                                                                                                                                                                                                99US-0277457.
                                                                                                                                                                                                                                                                                                                        24-MAR-2000; 2000WO-US07982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 272; Conservative
/*tag=
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB19149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rothenberg BE,
                                                                                                                                                                                 WO200058515-A1
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Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;
                                                                                                        (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                   Cullen LM, Jazwinska EC,
                                                                                                                                                           Disclosure; Page -; 32pp; English
                              autosomal recessive disorder; ss.
                                                                                                                                                                                                                                                                                                       y Match
Local Similarity 99.6%;
hes 272; Conservative
                                                                            97WO-AU00539
                                                                                       96AU-0002083
                                                                                             96AU-0001849
               Haemochromatosis gene.
                                                                                                                               WPI; 1998-179064/16.
   10-JUL-1998
                                                      WO9807884-A1
                                                                             22-AUG-1997;
                                                                                        03-SEP-1996;
                                            Homo sapiens
                                                                                             23-AUG-1996;
                                                                                                                    Busfield F,
                                                                  26-FEB-1998
                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 272
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241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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96US-0632673.
96US-0652265.
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                                                                                                        AAC68431 standard; DNA; 1440
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                                                                                                                                                                                    (first entry)
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ses 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIRA ) BIO-RAD LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-006341/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1996;
23-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-1996;
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                    21-FBB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feder JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                               AAC68431;
            528
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                                                                                      AAC68431
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        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the haemochromatosis (HC) gene. Mutations in this sequence are detected using the method of the invention. The method is for identifying an individual with hereditary haemochromatosis (HH) or a predisposition to develop HH or to genetically pass on HH to an offspring, comprising isolating a biological sample encompassing all or part of the DNA between markers D62265 and D62276, and detecting at least one homozygous or heterozygous mutation in a nucleotide within the region. The method can also be used for identifying an individual with an autosomal recessive disorder (ARD) or predisposition to develop and/or genetically pass on an ARD to an offspring, comprises isolating a biological sample from the individual and screening genomic DNA in the sample for the presence of a homozygous or heterozygous mutation in a gene, the normal function of which, is required to prevent progression of the disorder. The method(s) can be used to identify individuals that are homozygous or heterozygous (carriers) for the mutation causing the ARD. Especially the method is used to diagnose HH or predisposition to HH by detecting a Cys282Tyr substitution. Individuals homozygous for this mutation have HH and heterozygotes are potential carriers of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIGTGGCIGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 cécrrécrecerreacacretérécacracérerreareserecercadadadaden 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 gercririccrierricaagerrieggeraceregaecagecegererregar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of autosomal recessive disorder - particularly hereditary haemochromatosis, by detecting a mutation in the HC gene
                                                                 Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 271.4; DB 19; Length 2727; Pred. No. 3.6e-79; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                         Powell LW;
(first entry)
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121 CATGAGTGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ATGIGGCIGCAGCIGAGICAGAGICIGAAAGGGIGGGAICACAIGIICACIGIIGACIIC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 cecriectecerreacacrererecacracererreareserecteareserectra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 9.3e-79; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human hereditary hemochromatosis 24d2 mutation cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HH; hereditary hemochromatosis; chelation agent; r-cell differentiation factor; iron overload; ss.
273
                                              TGGACTATTATGGAAAATCACAAACCACAGCAAG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gnirke A, Ruddy D,
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0; Mismatches
       241 TGGACTATTATGGAAAATCACAACCACAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chelation agent alleviating iron overload
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4; 108pp; English
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3582 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 3641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated colon-specific nucleic acid molecule, useful for treating colon cancer, and diagnosing or monitoring the presence of metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3462 IGTITGAAGCITIGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTTCCT
                                                                                                                                                                                                                colon; cytostatic; vaccine; gene therapy; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5982 BP; 1659 A; 1247 C; 1518 G; 1556 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ^ Match 95.8%; Score 261.4; DB 25; Local Similarity 99.6%; Pred. No. 1e-75; Ne 262; Conservative 0; Mismatches 1; 1
   528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
                                                                                                                                                                                  Human colon specific nucleic acid, SEQ ID 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metastases of colon cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1, Page 155-156; 216pp; English.
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                                                                                    ВР
                                                                                                                                                                                                                                   colon disorder; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ghosh MG,
                                                                                    ABV93934 standard; DNA; 5982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of colon cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2001; 2001WO-US48414.
                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000; 2000US-244758P
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-018928/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sun Y, Recipon H,
                                                                                                                                                                                                                                                                                                 WO200277234-A2
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                   08-JAN-2003
                                                                                                                                                                                                                                                                                                                                  03-OCT-2002
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                                                                                                                    ABV93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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AAT96690
                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 GAIGAGAGICGCGIGIGGAGCCCCGAACICCAIGGGIIICCAGIAGAAITICAAGCCAG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ATGTGGCTGCAGCTGAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.8%; Score 269.8; DB 22; Length 1440; 99.3%; Pred. No. 9.3e-79; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuchihashi Z,
                                                                                                                                                                                                Human hereditary hemochromatosis 24d1/2 mutation cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1440 BP; 348 A; 354 C; 407 G; 331 T; 0 other;
                                                                                                                                                                                                                               HH; hereditary hemochromatosis; chelation agent;
T-cell differentiation factor; iron overload; ss
TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drayna DT, Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 4; 108pp; English.
                                                                                                  ВР
                                                                                                  AAC68432 standard; DNA; 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    llarity 99.3%;
Conservative
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96US-0652265.
                                                                                                                                                                 (first entry)
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nes 271; Conserv
                                                                                                                                                                                                                                                                                Homo sapiens
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23-MAY-1996;
                                                                                                                                                                                                                                                                                                                 US6140305-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WJ,
                                                                                                                                                                 21-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feder JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288
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                 528
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3461

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Gaps

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Length 5982;

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3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
extending from D6S265, which is a marker that is centromeric of extending from D6S265, which is a marker that is centromeric of tha.A., in a telemeric direction through D6S266, a marker at which the allelic association was no longer observed. A single mutation (24d1) in the HH gene appears responsible for the majority of HH (18ease. This comprises a G to A substitution that is present in 66% of affected chromosomes and in 4% of unaffected chromosomes. It results in a Cys to Tyr substitution in the encoded protein (see AM36499) at a critical disulphide bridge important for secondary structure. The following are claimed: the HH genomic DNA (1), a 1437 bp cDNA sequence (Ia) (see AAM36691) and their 24d1, 24d2 and 24d7, variants; a cloning or expression vector; host cells; a 24d7 variants; a cloning or expression vector; host cells; a 1437 bp cDNA sequence (Ia) (see AAM36691) and their 24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method residues of these; an antibody produced using the peptide; a method cell differentiation factors and therapeutic agents for the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigense oligomucleotide directed agai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 95.8%; Score 261.4; DB 18; Length 10825; Best Local Similarity 99.6%; Pred. No. 1.3e-75; Matches 262; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC68425 standard; DNA; 10825 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This genomic DNA sequence corresponds to the human gene whose mutated form is associated with hereditary hemmochromatosis (HH). To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HLA region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "G to A substitution (24d1 mutation associated with HH), results in Cys to Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'C to G substitution (24d2 mutation) results in His to Asp substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruddy D,
                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3; 115pp; English.
                                                                                                                    Hereditary haemochromatosis gene.
              AAT96690 standard; DNA; 10825
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5154..7106
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5882..6039
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Tsuchihashi Z, Wolff RK;
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P-PSDB; AAW36499.
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04-APR-1996;
16-APR-1996;
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3881

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Gaps

3821

04-APR-1997; 04-APR-1996; 16-APR-1996; 23-MAY-1996;

US6140305-A 31-OCT-2000 P-PSDB; AAB36869.

Thomas WJ,

Feder JN;

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TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGGGTC 3881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                       Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3762 GTTCACACTCTCTGCACTACCTCTTCATGGCTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                         Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic DNA of a histocompatibility iron loading (HFE) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cch 95.8%; Score 261.4; DB 22; al Similarity 99.6%; Pred. No. 1.3e-75; 262; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                            Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                  chelation agent alleviating iron overload -
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                                                                                                                                                                                                                                                            Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 3; 108pp; English.
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                                                                                                                          96US-0630912.
96US-0632673.
96US-0652265.
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                                                                                                                                                                                                                 (BIRA ) BIO-RAD LAB INC
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23-MAY-1996;
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US6140305-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                            Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                    New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.8%; Score 261.4; DB 22; Length 10825; 99.6%; Pred. No. 1.3e-75; cive 0; Mismatches 1; Indels 0; C
                                                                                                                                                                                                                                                            Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human hereditary hemochromatosis 24d1 mutation DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.
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96US-0632673.
96US-0652265.
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Query Match Best Loca Matches

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e.g. haemochromatosis, or a genetic susceptibility to develop it.
                      Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barton JC;
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               Location/Qualifiers
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10206..10637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metablolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF5; milk protein; Upus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; 88.
                                                                                                                                                                    4772 GCCGTGTGGGGCCCCGGACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGGCTGC
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                                                                                                                                          71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC
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                                                                                                                                                                                                                GCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTTCAAGCCAGATGTGGCTGC
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                                                                    11 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGGAGCAGGACCTTGGTCTTTCCT
                                   Gaps
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                                   0;
                                   Indels
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DB 21;
Score 261.4; DB 21;
Pred. No. 1.4e-75;
0; Mismatches 1;
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AAV57926/c
ID AAV57926 standard; DNA; 235033 BP.
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Ouery Match
Best Local Similarity 99.6%;
Matches 262; Conservative
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i Z, Wolff RK;
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WPI; 1998-240014/21

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haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual, and (b) assessing the
DNA or RNA for the presence or absence of a haplotype or genotype where
the presence or absence of the haplotype genotype indicates the likely
presence of the HFE gene mutation in the genome of the individual. The
Products from the present invention can be used to develop
products for use in the diagnosis and treatment of HFE. The present
invention also describes BTF genes, which are homologues of the milk
ordering butyrophilin (BT), and can be used in the production of agonists
and arteagonists of BT function. Also described are: (1) a RoRet gene
which can be used to develop products for the study, diagnosis and
treatment of lugus and Sjognen's syndrome; and (2) NPT3 and NPT4 genes
which are homologues of a type I sodium transport gene, and can
similarly be used for hypophosphatemia.
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43268 GCCGTGTGGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGGCTGC 43209 43329 43269 ó 71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130 131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250 43388 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGGACCTTGGTCTTTCCT 11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 0; Gaps Query Match
95.8%; Score 261.4; DB 19; Length 235033;
Best Local Similarity 99.6%; Pred. No. 4.8e-75;
Matches 262; Conservative 0; Mismatches 1; Indels 0; G Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other; 43148 rechanantenenacenenae 43126 251 TGGAAATCACAACCACAGCAAG 191 qq g à 셤 ð d ð ò

Hereditary haemochromatosis subregion from an HH affected individual AAV57903 standard; DNA; 237326 BP (first entry) Homo sapiens 21-DEC-1998 AAV57903; AAV57903/c RESULT 15

Bovine butyrophilin; BT; human hereditary haemochromatosis; HFB; diagmosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss.

39-APR-199B

97US-0852495. 97WO-US17658 30-SEP-1997; 07-MAY-1997; 01-OCT-1996;

(PROG-) PROGENTIOR INC.

Ruddy DA, Feder JN, Kronmal GS, Lauer PM, Isuchihashi Z, Wolff RK;

Thomas WJ;

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products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis (HFB) affected individual. Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual, and (b) assessing the bay or RNA for the presence or the haplotype genotype indicates the likely presence of the HFB gene mutation in the genome of the individual. The HFB gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFB. The present protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a ROREt gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type I sodium transport gene, and can can similarly be used for hypophosphatemia.
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                                          Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
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                                                                                                                                                                                     present invention describes hereditary haemochromatosis gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.8%; Score 261.4; DB 19; 99.6%; Pred. No. 4.9e-75; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 11, 2004, 18:33:14 Job time : 203.887 secs
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                                                                                                                                          Claim 1; Fig 9; 209pp; English
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                                                                                             metabolism
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: vinknown.>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,265
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/632,673
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
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GENERAL INFORMA
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Sequence 27, Appl
Sequence 1, Appli
Sequence 2, Appli
GENERAL INFORMA
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Sequence 9, Appli
Sequence 10, Appl
Sequence 1, Appli
Sequence 11, Appli
Sequence 12, Appli
GENERAL INFORMA
                                                                                                               February 11, 2004, 19:15:47; Search time 235.656 Seconds (without alignments) 4267.378 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/USO7_pUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_pUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-138-888-9
US-01-138-888-11
US-09-981-606-1
US-10-138-888-12
US-10-138-888-79
US-10-138-888-79
US-10-138-888-1
US-10-138-888-1
US-10-138-888-1
US-10-138-888-1
US-10-138-888-1
US-10-301-844-1
US-10-301-844-2
US-10-138-888-5
US-10-301-844-1
US-10-301-844-2
US-10-138-888-5
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                                                                                                                                                                                                                                                                                                                                2449703 seqs, 1841816367 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM nucleic - nucleic search, using sw model
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length: 2000000000
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Match Length DB
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	2	96	. ~	35.5	100		-10-272-665	Sequence	111,	App
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	4	4		15.7	4.6	12	-10-290-386-20	Sequence	207,	App
υ		4	. 60		585	13	-10-027-632-2	Sequence	7	5,1
υ			8.	15.3	585	14	-10-027-632-20996	Sequence	2099	5,
		4	ω.		9	12	8-934-8	Sequence	87,	App1
							ALIGNMENTS			
REUS	RESULT US-10-	RESULT 1 US-10-138-888-77 ; Sequence 77, A	388-77 77, Apj	plicat	77 Application US/10138	/101	38888			
	Pub G		INFOR	US20	0301489 N:	72A1				
••		APP	APPLICANT	T: The	aB,	Winston	_			
••				Dr	٠,'	Dennis	H .			
•• •				e c	Gnirke. A	John N. Andreas	. m			
- ••				Ruc	ddy, Da	David	1			
				TBI	Tsuchihashi,		Zenta			
		1	1		Wolff, Roger	ger				
		III			NTION:	Here	INVENTION: Hereditary Hemochromatosis Gene			
		NO.	NUMBER OF	NDENO	NUMBER OF SECOENCES: /	6/8				
			ADD	ADDRESSEE	E: Penni		Edmonds LLP			
٠.,			STR	EET:	STREET: 1155 Avenue	enne				
			CIT	Y: Net	CITY: New York					
			STA	STATE: New Y	STATE: New York					
			27.2	100	COUNTRI: USA 21P: 10036-2711					
		COM	PUTER	READ	COMPUTER READABLE FORM:	RM:				
			MED	MEDIUM TYPE:	YPE: F1	oppy	Floppy disk			
•			S C	COMPUTER:		υ	IBM PC compatible			
••			OPE	OPERATING		Σ + 	SYSTEM: PC-DOS/MS-DOS			
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COMPUTER READABLE FORM:
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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Pred. No. 1.8e-86;
; Mismatches 0; Indels 0;
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchinashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                              8907-095-999
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US-10-138-888-77
                                   NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/10138888 Publication No. US20030148972A1
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Best Local Similarity 100.0%; Po
Matches 273; Conservative 0;
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222..1268
                                                                                                                                                            INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
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STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /phenotype= "normal or wild-type
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                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30_CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04.APR-1997
APPLICATION NUMBER: US 08/652,265
                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                       FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: replace(408, OTHER INFORMATION: /phe (unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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LOCATION: replace(414,
OTHER INFORMATION: /phe
(unaffected)"
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TELEFAX: (212) 869-8864
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STRANDEDNESS: single
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99.4%;
ilarity 99.6%;
Conservative
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Best Local Similarity 99.6
Matches 272; Conservative
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; ORGANISM: Homo sapiens
US-09-981-606-1
Query Match
Best Local Similarity
Matches 272; Conserva
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 468 AIGIGGCIGCAGCIGAGTCAGAGTCTGAAAGGGTGGGAICACATGTICACTGTIGACTIC 527
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LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                     COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 12-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPAK: (212) 790-9090
TELEFAK: (212) 869-8864
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
IENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                               TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-138-888-10
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brian M. Poissant
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222..1268
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                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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Pred. No. 8.7e-86;
0; Mismatches 1; Indels 0;
                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation No. US20030129595A1

GENERAL INFORMATION:

APPLICANT: Rothenberg et al.

TITLE OF INVENTION: Mutations associated with iron disorders

TITLE OF INVENTION: Mutations 2002-10-16

CURRENT PELLING DATE: 2002-10-16

PRIOR PILING DATE: 1999-03-26

NUMBER CF SEQ ID NOS: 30

SOFTWARE: PARENTIN Ver. 2.1

SEQ ID NO. 1
DB 13; Length 1440;
Score 271.4; DB 13; Length
Pred. No. 6.9e-86;
0; Mismatches 1; Indels
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US-10-138-888-11
; Sequence 11, Application US/10138888
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121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                              408 GATGAGAGTCGCCGTGTGGAGCCCCGGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467
                                                                                                                                181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGGATCACATGTTCACTGTTGACTTC 240
                                                                                                                                                                              Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Folff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 04-APR-1997
FILING DATE: 23-MAY-1997
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brian M. POSSEMATION:
REFERENCE/DOCKET NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                       241 IGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                        528 resacrarraresaaarcacaacacaas 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: «UDKNOWT»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
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replace(408, "g")
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TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                          US-10-138-888-12; Sequence 12, Application US/10138888; Publication No. US20030148972A1; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thomas, Winston J. Drayna, Dennis T. Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.8%; Score 269.8; DB 13; Length 1440; Best Local Similarity 99.3%; Pred, No. 2.5e-85; Matches 271; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                      Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonde LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-271
COMPUTE READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/130, 868
FILING DATE: 02-May-2002
CLASSIFICATION TO APPLICATION OF APPLICATION DATA:

APPLICATION NUMBER: US 08/634,497
FILING DATE: 04-APR-1996
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: US 08/652,565
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TRLEPHONE: (212) 790-9090
                                           APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
                                                                                                                                                                              Tsuchihashi, Zenta
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LOCATION: replace(408,
OTHER INFORMATION: /phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-90
TELEFAX: (212) 869-8864
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Publication No. US20030148972A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                                                                                                                                                                                                                                                                                               CITY: New York
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                            NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
[HH]"
                                                                                                                                                                                                                                                                                                               Query Match 98.8%; Score 269.8; DB 13; Length 1440; Best Local Similarity 99.3%; Pred. No. 2.5e-85; Matches 271; Conservative 0; Mismatches
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Feder, John N.
Gnirke, Andreas
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 11.55 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 528 TGGACTATTATGGAAAATCACAACACAGGAAG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: AURHOWN:
PRIOR APPLICATION AURHER: US 08/834,497
APPLICATION NUMBER: US 08/652,265
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/652,265
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                    /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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APPLICANT: Thomas, Winston J.
                                                                             label= 24d2
                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                           US-10-138-888-12
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Sequence 25, Application US/10016634A

Sequence 25, Application US/10016634A

Publication No. US20020192666A1

GENERAL INFORMATION:

APPLICANT: Sun, Yongming

APPLICANT: Ghosh, Malavika

APPLICANT: Liu, Chenghua

TILLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Profitement and Applicant Methods Relating to Colon Specific Genes and Profitement and Applicant Methods Relating to Colon Specific Genes and Profitement Applicant Methods Relating to Colon Specific Genes and Profitement Applicant Methods Relating to Colon Specific Genes and Profitement Applicant Methods Relating to Colon Specific Genes and Profitement Applicant Methods Relating to Colon Specific Genes Applicant Methods Methods
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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Best Local Similarity 100.0%; Pred. No. 1.6e-82;
Matches 263; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 79.
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FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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                                                                                                                                        "Hereditary Hemochromatosis
                                                                                                                                                           (HH) protein"
/note= "No. US20030148972Almal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
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OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: replace(5834, "g")
OCHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.8%; Score 261.4; DB 13; Length Best Local Similarity 99.6%; Pred. No. 6.1e-82; Matches 262; Conservative 0; Mismatches 1; Indels
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Teuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                     REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEFRA: (212) 790-9090
TELEFRA: (212) 869-8864
OTHER INFORMATION: /product= "Heredit
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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APPLICANT: Thomas, Winston J.
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LOCATION: 5507..6023
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                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                           Score 261.4; DB 14; Length 5982; Pred. No. 4.7e-82; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feder, John N.
Gnirke, Andreas
Ruddy, David
Tauchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-MAY-2002
CLASSICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/652,265
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                                                                                    | FEATURE: | NAME/KEY: misc feature | LOCATION: (5885) | COTHER INFORMATION: n=a, c, g or t | US-10-016-634A-25
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                                                                                                                                                                                                                           95.8%;
FEATURE:
NAME/KEY: misc feature
LOCATION: (5780)..(5780)
OTHER INFORMATION: n=a, c,
                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.6'
Matches 262; Conservative
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LENGTH: 12146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.8%; Score 261.4; DB 13; Length 10825; Best Local Similarity 99.6%; Pred. No. 6.1e-82; Matches 262; Conservative 0; Mismatches 1; Indels 0;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                   SOFTWARE: Patentin Kelease #1.0, Version CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIPICATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
APPLICATION NUMBER: US 08/652,265
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-May-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
APPLICATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 28,907-095-999
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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gene 24d1 allele"
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LOCATION: 5507..6023
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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LOCATION:
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; Sequence 27, Application US/09981606; Publication No. US20030129595A1; GENERAL INFORMATION:

US-09-981-606-27

RESULT 11

APPLICANT: Rothenberg et al

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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.8%; Score 261.4; DB 13; Length 12146; Best Local Similarity 99.6%; Pred. No. 6.4e-82; Matches 262; Conservative 0; Mismatches 1; Indels 0;
TITLE OF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON CURRENT APPLICATION NUMBER: US/09/981,606 CURRENT FILING DATE: 2002-10-16 PRIOR APPLICATION NUMBER: 09/277,457 PRIOR FILING DATE: 1999-03-26 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver: 2.1 SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: <Unknown>
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
ATTORNEY/AGENT INFORMATION:
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ruddy, David A. Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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43338 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 43279
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                                                                                                                                                                                                                 Length 237326;
                                                                                                                                                                                                                                                               1; Indels
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Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                 DB 15;
                                                                                                                                                                                                                 Score 261.4; DB 1
Pred. No. 2.4e-81;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
PAPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
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APPLICATION NUMBER: US/10/138,888
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                                                                                                                               TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
IRLEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 237326 base pairs
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Thomas, Winston J.
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                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                      Best Local Similarity 99.6
Matches 262; Conservative
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                                                                                                                                                                        US-10-301-844-2
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US-10-138-888-5
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastESE for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION - CURROWN-
                                                                                                                                                                                                                                                        Score 261.4; DB 15;
Pred. No. 2.4e-81;
0; Mismatches 1; I
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
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ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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FILING DATE: 07-MAY-1997
                                                                                                                                                               TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-493-5556
TELEFX: 66141 PENNIE
INFORMATION FOR EEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 23503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                               Matches 262; Conservative
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ZIP: 10036-2811
                                                                                                                                                                                                                                                                            Best Local Similarity
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PRIOR APPLICATION DATA:
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                                                                          (HH) protein containing the 24d2
                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 10825
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Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKNOWn>
                                                                                                                                                        /note= "Hereditary Hemochromatosis (HH)
                                                                                                                                                                                                                                                                                                                                                     95.2%; Score 259.8; DB 1: 99.2%; Pred. No. 2.3e-81;
             REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPAK: (212) 790-9090
TELEPAK: (212) 869-8864
OTHER INFORMATION: /product= "Heredit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                       NAME/KEY: -
LOCATION: 5507..6023
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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US-10-138-888-7
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
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MEDIUM TYPE: Floppy disk
 NAME: Brian M. Poissant
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
ATTORNEY AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTRATION NUMBER: 28 462
REFERENCE/DOCKET UNWER: 8907-095-999
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 780-9090
TELEPHONE: (212) 780-9090
TELEPHONE: (212) 869-8864
OTHER INFORMATION: /product= "Hereditar: (HH) protein containing both the 24d1 and 24d2 mutations"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
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SEQUENCE DESCRIPTION: SEQ ID NO:
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Best Local Similarity 99.2%;
Matches 261; Conservative
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LOCATION:
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February 11, 2004, 15:39:51 ; Search time 904.219 Seconds (without alignments) 6831.698 Million cell updates/sec
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1 aacatcaccatgaagtggct.....gcagagatatacgtnccagg 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description.	AR097991 Sequence AR117804 Sequence AR117804 Sequence AR117805 Sequence AR117805 Sequence AR117805 Sequence AR117805 Sequence 182157 Sequence 13 182158 Sequence 23 182158 Sequence 34 1821549 Homo sapi AR079409 Homo sapi AR149407 Homo sapi AR117795 Sequence AR117795 Sequence AR117795 Sequence AR117795 Sequence AR117795 Sequence AR117795 Sequence AR117790 Sequence AR117791 Sequence AR14760 Penn Represence AR14760 Pe	linear PAT 14-FEB-2001
ΙD	AR097991 AF525359 AR117804 AR117804 AR117804 AR149475 AR149475 AR149475 182157 182157 182157 182157 182157 182154 AF079409 AF079409 AF079409 AF079409 AF115265 AF079409 AF11739 AR117794 AR117794 AR117790 AR117790 AR117790 AR117790 AR117790 AR117790 AR117790 AR117790 AR117790 AR117790 AR117790 AR117790 AR117790 AR149465 AR149461 AR149461 AR149461 AR117790 AR117790 AR149461 AR149461 AR149461 AR149461 AR117790	360 bp DNR US 6074825. 8 C.P.H. C.P.H. 13-JUN-2000;
% Query ore Match Length DB	150 150 150 150 150 150 150 150	AR097991 Sequence 5 from patent AR097991 Unknown. Unknown. Unclassified. 1 (bases 1 to 360) 1 (bases 1 to 360) Stable encapsulated reparted reparte
Result No. Scr	0 111111111111111111111111111111111111	RESULT 1 AR097991 LOCUS. DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES

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AR117805
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KEYWORDS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 479)
Kutlar,F., Glendenning,M. and Kutlar,A.
Heterozygote C-->G mutation in intron 3 of human hemachromatosis gene detected on a caucasian individual with beta thalassemia trait Unpublished
                                                                                                                                                                                                                                                                                                                                    Home sapiens hereditary hemochromatosis protein HLA-H precursor AF525359
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Kutlar, F., Glendenning, M. and Kutlar, A.

Kutlar, F., Glendenning, M. and Kutlar, A.

Submitted (27-JUN-2002) Medicine/Hematology-Oncology/Hemoglobin DNA
Laboratcory, Medical College of Georgia, 15th Street, AC-1000,
Augusta, GA 30912, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAM82608.1"
/db_xref="G1:21952518"
/translation="PPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKE
                                                                                                    0;
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precursor"
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Pred. No. 2e-36;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="6"
             /organism="unknown"
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/sex="male"
                                                                     99.3%;
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/gene="HFE"
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Matches 150; Conservative
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I (Dases 1 to 517)
Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z. and Wolff, R.K.
FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIW'
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Pred. No. 2e-36;
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Patent: US 6140305-A 20 31-OCT-2000;
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Sequence 20 from patent US 6140305.
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Sequence 21 from patent US 6140305.
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/gene="HFE"
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Matches 150; Conservative
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 20 08-MAY-2001;
Location/Qualifiers
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
Hereditary herochromatosis gene products
Patent: US 6140305-A 21 31-0CT-2000;
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Pred. No. 2e-36;
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Seguence 21 from patent US 6228594.
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                                                    Location/Qualifiers
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PAT 10-JUN-1998
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              Unclassified.

1 (bases 1 to 517)

Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Fsuchihashi, Z. and Wolff, R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 21_08-MAY-2001;
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Tsuchihashi,Z., Gnirke,A., Thomas,W.J., Drayna,D.T., Ruddy,D.,Wolff,R.K. and Feder,J.N.
Hereditary hemochromatosis diagnostic markers and diagnostic
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Pred. No. 2e-36;
0; Mismatches 1; Indels
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Location/Qualifiers
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Tsuchihashi,Z., Gnirke,A., Thomas,W.J., Drayna,D.T., Ruddy,D., Wolff,R.K. and Feder,J.N.
Hereditary hemochromatosis diagnostic markers and diagnostic methods
Patent: US 5712098-A 13 27-JAN-1998;
                                                                                                            1 (bases 1 to 517)
Tsuchihashi,Z., Ghirke,A., Thomas,W.J., Drayna,D.T., Ruddy,D.,
Wolff,R.K. and Feder,J.N.
Hereditary hemochromatosis diagnostic markers and diagnostic
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Sequence 13 from patent US 5712098.
182167
182167.1 GI:3210464
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Location/Qualifiers
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 182158 517 bp
Sequence 4 from patent US 5712098.
                                                                                                                                                                                                        1. .517
/organism="unknown"
120 c 146 g
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120 c 146 a
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                                         I82158.1 GI:3210455
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Best Local Similarity 99.3%
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/codon_start=3
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                                                                                                                                                                                                                                                                                Lutlar, F., Holley, L., Glendenning, M. and Kutlar, A. A new compound heterozygotes IVS4-48G/A/IVS4-115T/C polymorphism of HFE gene found in an Africa American individual with mild anemia Unpublished
                                 PRI 07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 551)
KutLar,F., Holley,L., Glendenning,M. and Kutlar,A.
Direct Submission
Submitted (21-DEC-2000) Medicine/Hemoglobin DNA Laboratory; Sickle Cell Center, Medical College of Georgia, 15th street, AC-1000
                                                                                                                                                                                                               Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
551 bp DNA linear PRI 07-MAR-Homo Sapiens hereditary hemochromatosis protein precursor (HFE) AF331065
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/note="HLA-H precursor; putative iron-binding ligand</pre>
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/note="heterozygous polymorphism"
/replace="t" 153 g 141 t
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'replace="g"
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/cell_type="WBC"
/tissue_type="whole_blood"
<1. .>551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .551
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="6"
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                                                                                                                             AF331065.1 GI:13241987
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<1. .116
/gene="HFE"
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/gene="HFE"
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/gene≈"HFE"
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/gene="HFE"
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Homo sapiens hereditary hemochromatosis protein precursor (HFE)
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FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIG
VISGIAVFVVILFIGILFIILRKRQGS"
194 AAAGACGTATTGCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 253
                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 733)
Kutlar,F., Glendenning,M. and Kutlar,A.
Heterozygote T->C mutation was detected at the intron 4 of thuman hemachromatosis gene in an Africa American individual
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|oin(<114. .389,548. .>661)
|gene="HFE"
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gene="HFE"
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'note="heterozygote"
'replace="t"
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replace="a"
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/cell_type="WBC"
<1. .>733
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'gene="HFE"
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Gasparini, P.
Direct Submission
Submitted (04-DEC-1996) P. Gasparini, Servizio de Genetica Medica -
IRCCS, 'Ospedale CSS', Via Cappuccini, 71013 S Giovanni, Rotondo
(FG), ITALY
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                       1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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               Score 150; DB 9; Length 551;
Pred. No. 2e-36;
0; Mismatches 1; Indels
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    .653
    /organism="Homo sapiens"

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/db_xref="taxon:9606"
/map="6p22"
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/usedin=Y09801:hfe_mrna
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/usedin=Y09801:hfe_mrna
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H.sapiens HFE gene, exon 4 &
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                     Query Match
Best Local Similarity 99.3%;
Matches 150; Conservative
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51. .326
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/gene="HFE"
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51. .598
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Submitted (21-JUL-1998) Immunology, University of Cambridge, Tennis Court Road, Cambridge CB2 1QP, UK Location/Qualifiers
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/protein id="AACC2648.1"
/db xxef="G1:3695111"
/translation="WORRARRALLLIMLLQTAVLQCRLLQSHTLQVILGCEMQEDNST
BGYWKYGYDGQDHLBFCPDTLDWRAAEPRAMPTKLEWERHYIRARQNRAYLERDCPAQ
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TYGGHITLAYPPGEGRYTCQVEHFGLDQPLIVIWEPSPSGTLVIGVISGIAVFVVII
FIGILFIILRKRQSSRGAMGHYVLAERE"
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HOMO Sapiens Hemochromatosis splice variant delE2(14E4) (HFE) mRNA, complete cds.
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Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                               1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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Abdes, D.A. and Trowsdale, J. Ahternate splice variants of the hemochromatosis gene Hfe Immunogenetics 49 (4), 357-359 (1999)
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Pred. No. 2e-36;
0; Mismatches 1;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
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 note="homozygous"
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/codon_start=1
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1. .781
               /replace="a"
564 677
/gene="HFE"
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37. .777
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167 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tränslation="PPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKE
FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIG
VISGIAVFVVILFIGILFIILRKRQGS"
                                                                                                                                                                                                                                                                                                                                        PRI 05-0CT-1999
                   o,
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                                                                                        197 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 256
                                                                                                                                                               257 AAAGACGTATTGCCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 316
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 772)
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/codon_start=3
/product="hereditary haemochromatosis protein precursor"
/protein id="AAF01222.1"
/db xref="G1:6010711"
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens hereditary haemochromatosis protein precursor (HFE)
                                                       1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                 AAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kutlar, F., Sromek, E., Holley, L., Leithner, C., Nechtman, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kutlar, F., Sromek, E., Holley, L., Leithner, C., Nechtman, J. and
                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two different mutations found in intron 4 of the human hemochromatosis gene, in a Turkish family Unpublished
                                                                                                                                                                                                                                                                                                                                      linear
                 Indels
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                                                                                                                                                                                                                                                                                                                                        DNA
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/cell_type="white blood cell"
<1. .>772
Pred. No. 2e-36;
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join(<130. .405,564. .>677)
/gene="HFE"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
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380 AAAGACGTATTGCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 439
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Job time : 905.219 secs
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Submitted (04-NOV-1999) Oliva R., Human Genome Research Group,
Faculty of Medicine and Clinic Hospital, Casanova 143, 08036, SPAIN
Location/Qualifiers
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CRALNYYPQNITMKWLKDXQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEGRYTC
QVEHPGLDQPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFIILRKRQGSRGAMG
                                                                                                                                                                                                                                                                                                                                  HSA250635 809 bp mRNA linear PRI 03-NOV-2001
Homo sapiens mRNA for Hemochromatosis protein (HFE gene), DELEX2+3
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                                                                            430 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                   61 AAAGACGTATIGCCCAAIGGGGAIGGGACCIACCAGGGCIGGAIAACCTIGGCIGIACCC
                                    1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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/protein_id="CAC80805.1"
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/cell line="HepG2"
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Sequence:

Searched:

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AZ074811 RPCI-23-4
BA7025784 RPCI-23-3
BA7025784 RPCI-23-3
BA7025010 Mus muscu
AK030595 Mus muscu
AK020594 Mosee gen
CB466784 702494 Mb
BF118828 601755052
BQ88942 AGENCOURT
CB221873 11621A5
BPR28080 MR1-HN007
CB222669 11130E11
BE481497 176270 BA
BX437832 RC5-0T009
AA475498 VA15.65.r
CB530229 737006 MA
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CB530229 AGENCOURT
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BF741057 QV1-HB003
BF171757 PCL3324 M
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov Plate: LLCM240 row: j column: 04
High quality sequence stop: 566.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Email: cgapbs-r@mail.nih.gov
Email: ccapbs-r@mail.nih.gov
CDN Library Preparation: Ling Hong/Rubin Laboratory
CDN Library Preparation: Ling Hong/Rubin Laboratory
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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      BE272926 601171213
BM723847 UI-E-E01-
CB529554 UI-H-FT2-
BG747345 602704818
                                                                                                                   February 11, 2004, 15:39:52 ; Search time 861.127 Seconds (without alignments) 4261.827 Million cell updates/sec
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Compugen Ltd.
                                                                                                                                                                                                                                                                                                  22781392 seqs, 12152238056 residues
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                        GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                      nucleic search, using sw model
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/done libe Wille recommonstates (i. phase resistance)
/done libe Wille Notice recommonstates (Transparents)
/done libe Wille Wetcor: pT773-Peo (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
UI-E-EO1 is a normalized cDNA library containing the UI-E-EO1 is a normalized cDNA library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, dispested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTMARCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
                                                                      /dev stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                       clone="UI-E-E01-aix-h-17-0-UI"
                                                 type="fetal eye"
  db xref="taxon:9606"
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                                                                                                           /tissue_rimachisourcell adenocarcinoma"
/tissue_rype="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH1 MGC_14"
/clone_lib="NH1 MGC_14"
/note="Organ: kidney; Vector: pOTB7; Site_l: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >SOODp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 668)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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UI-E-EO1-aix-h-17-0-UI.rl UI-E-EO1 Homo sapiens CDNA clone
UI-E-EO1-aix-h-17-0-UI 5', mRNA sequence.
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University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.3%; Score 150; DB 10; Length 570; 99.3%; Pred. No. 5.8e-33; Arive 0; Mismatches 1; Indels
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                       organism="Homo sapiens"
                                                                                              clone="IMAGE:3544803"
                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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CB529554 Iinear EST 16-MAY-2003
UI-H-FT2-bjh-m-12-0-UI.sl NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjh-m-12-0-UI 3', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Lolen Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: Mil FORWARD
POLYA-Yes.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases 1 to 729)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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                                                                                Gaps
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       Length 668;
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Score 150; DB 12;
Pred. No. 6.2e-33;
0; Mismatches 1;
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Query Match
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 819)
WIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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blate: LLCM1711 row: d column: 06
High quality sequence stop: 792.
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TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEO=GGCCATGCG"
211 c 165 g 202 t
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/db_xref="taxon:9606"
/clone="lmAGE:4857941"
/tissue_type="adenocarcinoma cell line"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
                                                                      tissue type="Aveolar Macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 150; DB 14;
Pred. No. 6.4e-33;
0; Mismatches 1;
/db_xref="taxon:9606"
/clone="UI-H.FT2-bjh-m-12-0-UI"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Matches 150; Conservative
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Department of Eukaryotic Genomics
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The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@eijar.ozg
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgon.com). BAC end page:
http://www.iigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 316 row: A column: 10
Seq primer: T7
Class: BAC ends.
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Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Wouse BAC End Sequences from Library RPCI-23
Unpublished
/note="Organ: colon, Vector: pOTB7; Site 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)" a 201 c 235 g 181 t
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 5.7e-26;
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/strain="C57BL/6J"
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/clone="RPCI-23-316A10"
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/clone_lib="RPCI-23"
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Matches 148; Conservative
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ECORI; Site 2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACG3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Nas musculus 2 days neonate thymus thymic calls cDNA, RIKEN
full-length enriched library, clone:E430034019
product:hemochromatosis, full insert sequence.
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                                                                                                                                                                                                                                                 Match 55.9%; Score 84.4; DB 28; Local Similarity 72.2%; Pred. No. 4.6e-14; les 109; Conservative 0; Mismatches 42;
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ligh-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuki, R., Aono, H., Baldarelli, R., Barsh, G., Blacke, J., Boffelli, D., Bolunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fulita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Rang, B., Ringwald, M., Rodriguez, T., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L., Wynshaw, Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection
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/tissue type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Displaying the control of the contro
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Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1719)
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/db_xref="taxon:10090"
/clone="E430034J19"
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/strain="NOD"
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Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310032M04 product:hemochromatosis, full insert
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/protein_id="BAC40688.1"
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                                                                                                                PKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLELGRGVLGQQVP
TYKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKYLDNGDETYQ
GWLTLAVAPGDETRFTCQVERFEGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVGI
LFLILRKRKASGGTWGGYVLTDCE"
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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PTLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVLPNGDETY
QGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVG
                                     'tissue_type="tongue"
'clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                               DLGLPLFEARGYVDDQLFVSYNHESRRAEPRAPWILEQTSQLWLHLSQSLKGWDYMF
IVDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWRYGYDGQDHLEF
                                                                                                                                                                                                                                               translation="MSLSAGLPVRPLLLLLLWSVAPQALPPRSHSLRYLFMGASEP"
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1 (bases 1 to 831)
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11629 row: j column: 20
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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(MGD|MGI:109191)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 84.4; Db .r., ...d. No. 7.8e-14; .... 42; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 7.8e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 954 ccresesaccasecraserreaccrercase 984
                                                                                                                                                                                                                                                                                                                                                            ILFLILRKRKASGGTMGGYVLTDCE"
                                                                                                                                                                                       /protein_id="BAB26373.1"
/db_xref="GI:12844463"
/db_xref="MGI:109191"
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Location/Qualifiers
                                                                     dev stage="adult"
clone="2310032M04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        454
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                 /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative"
                                                                                                                                                                        codon start=1
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                                                                                                                                                                                                                                                                                                                                                                             1695. .1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 c
                                                                                                                                                      putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 polyA_site
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Best Local
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AUTHORS
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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BI452668
LOCUS
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Other_GSSS: RPCI-23-408J22.TV
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pietradejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://papac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALOVABIL 536 bp DNA linear GSS 31-MAR-2000 RPCI-23-408J22.TJ RPCI-23 Mus musculus genomic clone RPCI-23-408J22 , genomic survey sequence.
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Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 536)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
, B., Levina, M., Mogann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                             /clone lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCNV-SPORT6; Site 1: Sal1;
Site 2: Not1; Cloned unidirectionally. Primer: Öligo dr.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 CAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TAACGGGGATGAGACCTATCAAGGCTGACATTGGCCGTGGCCCCTGGGGACGAGAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 GTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
/mol_type="mRNA"
/grzaln="CSTBL/6J"
/db xref="taxon:10090"
/clone="IMAGE:5249395"
/tissue type="tumor, gross tissue"
/dev stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BAC End Sequences from Library RPCI-23 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.7%; Score 73.6; DB 12; 70.8%; Pred. No. 7.7e-11; iive 0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                        215 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                    189 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 AAGGITCACCIGICAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 GAGATATACGINCCAGG 151
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/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3 6; Site 1:
Fore 1: Site 2: EcoR1; Female C57BL/65 mouse kidney and/or
Broin; Site 2: EcoR1; Female C57BL/65 mouse kidney and/or
Brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
a 135 c 112 g 108 t
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Mammalia; Butheria; Perissodactyla; Equidae; Equus.
1 (bases 1 to 473)
Watson,J.L., Vandenplas,M., Cordonnier-Pratt,M.-M., Sudman,M.,
Wentzel,V., Gingle,A., Moore,J. and Pratt,L.H.
An EST database from equine (Equus caballus) mesenteric lymph nodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Equus caballus"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/clone lib="Mesenteric lymph node (MLNI)"
/note="Organ: Mesenteric lymph node; Vector: pBluescript
SK(-) from Lambda ZapII; Site_1: EcoRI; Site_2: EcoRI; The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM781326 473 bp mRNA linear EST 05-MAR-2002 MLN1 7_F05.g1_A005 Mesenteric lymph node (MLN1) Equus caballus cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 AACATCACTATGAGGTGGATGAAGGACAACCACTGGATGCCAAAGATGTCAACCCC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences have been trimmed to exclude PolyA, vector and regions below Phraed quality 16. The threshold for high quality sequence is 20. The cDNAs were cloned non-directionally such that the primer used for sequencing has no bearing on whether it is a 3' or 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tal: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65.6; DB 28; Length 481; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 CCTGGGGACGAGACAAGGTTCACCTGTCAAG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
/db_xref="taxon:10090"
/clone="RPCI-23-316C10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 2
High quality sequence stop: 473
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                                                                                                                 /lab_host="DH10B"
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                                                                            /sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equus caballus (horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
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BM781326/c
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                                                                                                                                                         /lab host="unioud" // clone lib="RPCI-23" // clone lib="RPCI-23" // clone lib="RPCI-23" // clone lib="RPCI-23" // note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: BCORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " 124 q 114 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ025784 481 bp DNA linear GSS 25-FEB-2000
RPCI-23-316C10.TV RPCI-23 Mus musculus genomic clone RPCI-23-316C10
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Mouse BAC End Sequences from Library RPCI-23
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Clones are derived from the mouse BAC library RPCI-23. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

seg primer: 17
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 481)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 28; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70.8; DB 28; Length 53
Pred. No. 4.2e-10;
0; Mismatches 43; Indels
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Other GSSs: RPCI-23-316C10.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
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/mol type="qenomic DNA"
                                    /db_xref="taxon:10090"
/clone="RPCI-23-408J22"
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/strain="C57BL/6J"
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Matches 107; Conservative
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library was made from poly-A RNA in the cloning vector lambda ZAPII. Clones to be sequenced were prepared by mass excision." 147 c 132 g 91 t
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                                                                                                                                                                                                                                                                                                              361 CACTCTGACCTGGCTTCTGGATGGGGAGCCCATGCACCAGGGCACCTTTGGGCCTAGGGC 302
                                                                                                                                                                                                                                                                                                                                                               66 CGTATTGCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCTGG 125
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                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                           6 CACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGA
                                                                                                                                                                                                                Gaps
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                                                                                                                                                    Score 52.2; DB 12; Length 473; Pred. No. 9.4e-05;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fulta, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Iyons, P., Harman, M., Hume, D.A., Kamiya, M., Lee, N.H., Iyons, P., Marchioni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Sting, B., Ringwald, M., Rodriguez, T., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Mang, K.H., Weltz, C., Whittaker, C., Wilming, L., Wanshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Ishili, Y., Itch, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Miyazaki, A., Murata, M., Okazaki, Y., Saito, R., Saito, H., Sasai, K., Sakai, K., Sakazume, N., Sano, H., Sasai, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tagami, M., Towaru, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.
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Enx:81-45-503-9216
Enxylopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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/db_xref="G1:26326681"
/translation="Wilsbrikalaalhimivyliledliggrcaegdnorlyasapyo
/translation="Wilsbrikalaalhimivyliledliggrcaegdnorlyasapyo
prianslatichervoalaephtirydimalslevpglepeltitryfddeperlykkkossir
bsogprikchiraeptwykkerddlogebebgolkgmiaeltagwogontdihilgarfeggel
orngstrgfwkigydgonflifpdyktiffwtydgpstgknytimktraapradlukafid
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2338)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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URL.http://genome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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'db_xref="taxon:10090"
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/strain="C57BL/6J"
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Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Kueh.P., Lewis,S., Matsudo,T., Gissi,C., King,B., Kochiwa,H., Kueh.P., Lewis,S., Matsudo,T., Pascalole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Batsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Hill,D., Marchionni,L., Mashima,J., Mazzarelli,J., Mombachts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Toyo-oka,K., Wanng,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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E (bases 1 to 2490)

Radachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hachizume,W., Hayashida,K., Hayatsu,N., Hiramcto,K., Hiracka,T., Hirozane,T., Hori,F., Imocani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakamura,M., Nishi,K., Nomura,K., Nunyazaki,A., Murata,M., Nishi,K., Nomura,K., Nunyazaki,A., Murata,M., Okazaki,Y., Saito,R., Saito,R., Saito,R., Saito,R., Sakai,C., Sakai,K., Sakai,C., Sakai,K., Sakaine,N., Sagabe,Y., Tagawa,A., Takahashi,F., Tahaku,A., Tanaka,T., Tomaru,A., Takahashi,F., Takaku-Akahira,S., Muranta,M., Takahashi,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'tissue_type="skin"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
            Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product; hypothetical Major histocompatibility complex protein, Class I containing protein (InterPro|IPR001039, evidence: InterPro)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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Please visit our web site for further details.
URL:http://fantome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/clone="4732481C10"
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/strain="C57BL/6J"
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YRKPVQQKTFGSETILPSGDGTYQAWVSIRVLPGQESQFSCNLKHGNHNINEPAATEA
PVYGARREQPPTSGVGSRVGKSLWSAMTTALVVISWTLSQKLMGPLLWFCSGGFCSFL
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Best Local Similarity 62.7%;
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VERSION
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/db_xref="G1:26324972"

/db_xref="G1:26324972"

/tanalation="MILSRNIRALAAIHLMIVYLLLEDLLGTCAEGDNQRLVASAPYQ

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QRNGSTRGFWKLGYDGQNFLTPDQKTLTWTVDGPSTTQKNKTPWKTRAPRADIVKTFLD

DCPAQLQRYLASLRNGLHTGPPKVILVYFRNYPVGRITLTCARRIYYTWATLTWLQ

YRKPVQQKTFGSETLILBSGDGTYQAWYSIRVLPGGBSTGRGRGRGRHNINIREAATER

PVYGARREQPPTSGVGSRVGKSLWSAMTTALVVISWTLSQKLLGFLLMFCSGGFCSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-JUL-1997) Masayasu Yoshino, U.T. Southwestern Medical Center, HHMI; 5323 Harry Hines Blvd, Dallas, TX 75235-9050, USA (E-mail:YOSHINO@UTSW.SWMED.EDU, Tel:214-648-5047, Fax:214-648-5453)
                                                                                                                                                                                                                                                                                                                                                         1074 CACCCTGACCTGGCTTCAGTATAGAAAGCCAGTACAGCAGAAAACCTTTGGATCTGAAAC 1133
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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196 c 198 g 192 t 5 others
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Pred. No. 0.00055;
0; Mismatches 53;
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/organism="Mus musculus"
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/strain="BALB/c"
/db_xref="taxon:10090"
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/clone="cosmid 12.1"
/haplotype="H2d"
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llarity 62.7%;
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2 ACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTA 61

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Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
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                                                                           62 AAGACGIAITGCCCAAIGGGAIGGGACCIACCAGGGCIGGAIAACCITGGCIGTACCCC 121
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1 (bases 1 to 710)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593 cccaddacarogagcrigrogagaccaggccrrcaggggriggaaccrrcagaagriggg
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Best Local Similarity 65.4%; Pred. No. 0.0014;
Matches 70; Conservative 0; Mismatches 37; Indels 0;
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732494 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
CB466784
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                                                                                                                                                                                   122 CTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                         341 TTGGGAAAGAGCAGAGTTACACATGCCATG 370
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Seg primer: GTAATACGACTCACTATAGGG.
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/organism="Bos taurus"
/mol type="mRNA"
/db xref="taxon:9913"
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Contact: Smith TPL
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> AAF58227 ABK83570

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AAV5790;

148.4 51 AAH02415 AAH02416

ABQ78762 AAI63974

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ABX39656 AAQ12117 ABX63563 AAI93004 ABZ11436

434 1101 1377 1554

AA16397

Bovine EST associa HLA-C exon Cb-2. Human CDNA #563 di Human polynucleoti

Human polynucleoti Human polynucleoti Human polynucleoti Human breast cell Human foetal liver Probe #14690 for g Human bone marrow Probe #14109 for g Probe #14109 for g Probe #19729 used t Human liver single

> AAK43395 AAI24176

AAI49463 AAI09738 ABS43016

ABA51289 ABA69295 ABA36224

AAI64011

Hereditary haemoch Human hereditary h Human hereditary h Human hereditary h Human hereditary h Genomic DNA of a h

AAC68428

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AAA96769 AAV23525

Human hereditary

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Hereditary hemochromatosis gene; encapsulate; lipoprotein outer membrane; membrane; senembrane stability; test cell; molecular diagnosis; genetic testing; ss.
                                                                                                                                                                                                                                                                                                                                                              Biological preparation of a stably encapsulated reference nucleic
                                                                                                                   Hereditary hemochromatosis gene target nucleic acid sequence.
ALIGNMENTS
                                                   AAX16055 standard; DNA; 359
                                                                                                                                                                                                                                         98WO-US15641
                                                                                                                                                                                                                                                             97US-0997522
                                                                                                                                                                                                                                                                         97US-0905124
                                                                                                                                                                                                                                                                                             (MAIN-) MAINE MEDICAL CENT.
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                   Rundell CA, Vary CPH;
                                                                                                                                                                                                                                                                                                                                          WPI; 1999-153816/13.
                                                                                              19-MAY-1999
                                                                                                                                                                        Unidentified
                                                                                                                                                                                              WO9906594-A1
                                                                                                                                                                                                                                       29-JUL-1998;
                                                                                                                                                                                                                                                             23-DEC-1997;
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ID AAC6
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                                         The present sequence represents a nucleic acid sequence that is used as a reference sequence to exemplify the method of the invention. The specification describes a method for the biological preparation of a stably encapsulated reference nucleic acid for molecular diagnostic and genetic testing. The method comprises inserting a vector containing a reference nucleic acid into a cell through its lipoprotein outer membrane to encapsulate the nucleic acid, multiplying the cell to propagate the nucleic acid, multiplying the cell to propagate the and achieving a desired stability of the cell membrane for substantially matching the nucleic acid with the membrane stability of test cells. The reference nucleic acid with the membrane stability of test cells. The
                                                                                                                                                                                                                                                                                                                        AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                                                                                                                                                                                                                                                                                                     173
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                                                                                                                                                                                                                            Length 359;
 for molecular diagnostic and genetic testing
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                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                   Sequence 359 BP; 86 A; 91 C; 101 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HH; hereditary hemochromatosis; chelation agent;
T-cell differentiation factor; iron overload; 88.
                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                         1.1e-39
                                                                                                                                                                                                                                                                                                                                                                       CCTGGGGAAGAGAGATATACGTNCCAGG 151
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                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                              Score 150;
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                       5; Page 48; 51pp; English
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96US-0632673.
96US-0652265.
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Les 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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23-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                 174
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                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                         61
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                      Claim
acid
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New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal

chelation agent alleviating iron overload

Disclosure; Fig 6; 108pp; English

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                                                                                                                                                                                                                                                                                                                               243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                                                                                                                                                                                                                                                                   183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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products. These proteins may be used to treat a patient diagnosed a having human hemochromatosis disease. It is also useful as a metal callediation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replace therapy for individuals having a defective human hemochromatosis ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human hereditary hemochromatosis DNA used for mutation detection.
                                                                                                                                                                                              0
                                                                                                                                                      Score 150; DB 22; Length 517; Pred. No. 1.2e-39; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsuchihashi Z,
                                                                                                                 Sequence 517 BP; 126 A; 120 C; 147 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 517 BP; 127 A; 120 C; 146 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HH; hereditary hemochromatosis; chelation agent;
T-cell differentiation factor; iron overload; ss
                                                                                                                                                                                                                                                                                                                                                                                                                        333
                                                                                                                                                                                                                                                                                                                                                                                121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                              303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 6, 108pp; English
                                                                                                                                                      99.3%;
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96US-0632673.
96US-0652265.
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                                                                                                                                                                                          150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-006341/01.
                                                                                                                                                    Query Match
Best Local Similarity
Matches 150; Conserv
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23-MAY-1996;
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                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      iron absorption regulator; intracellular iron absorption; lung injury; haemochromatosis; transfusion; thalassaemia; haemolytic anaemia; chronic infection; transferrin receptor; IfR; brain tumour; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by
                                                                                                                             AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                                                              AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                            183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
                               o;
   Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxidative stress disorder; tissue damage; vascular disease; inflammation; atherosclerosis; autoimmune disease; inflammatory condition; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
                               Indels
                                 ٦;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "beta2M/HFE monochain"
Score 150; DB 22;
Pred. No. 1.2e-39;
0; Mismatches 1;
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                                                                                                                                                                                             121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                      303 CCTGGGGAAGAGAGAGATATACGTACCAGG 333
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                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                                          ABK49917 standard; cDNA; 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rotem-Yehudar R,
 99.3%;
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                al Similarity 99.3
150; Conservative
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   Query Match
Best Local
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ABK49917
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thalassaemias, haemolytic anaemia or chronic infections, and for delivering a therapeutic to cells that over-express transferrin receptor (TFR) which are preferably lymphocytes or leukocytes, across the bloodcomain barrier. (I) is further useful for treating brain tumour. (I) is also useful for treating oxidative stress disorders resulting in tissue damage e.g. vascular diseases, inflammation, atherosclerosis, lung injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful as a platform for drug delivery of therapeutic use for cancer, autoimmune diseases and inflammatory conditions. The monochain manifests specific characteristics advantageous for drug delivery systems. It is a coluble, stable and fully conformed protein. It binds specifically to transferrin receptor (TFR) and therefore targets cells that over-express this receptor. It is continuously internalised by the target cells, thus cells, minimising side effects. It dissociates from the receptor in the cells, minimising side effects. It megatively regulares iron absorption, reducing growth of undesired cells and preventing lymphocyte activation. It is not diluted in the blood as is transferrin. It should not induce an immune response since it is a self non-polymeric protein and delivery of drugs via monochain is expected to overcome drug-resistance since it is a continuous of heterometric represents the continuous of heterometric represents the
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"G to A substitution (24dl mutation
associated with HH), results in Cys to
Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1317;
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"C to G substitution (24d2 mutation)
results in His to Asp substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              results in Ser to Cys substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A to T substitution (24d7 variant)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 150; DB 24;
Pred. No. 1.6e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                  coding sequence of beta2m/HFE monochain.
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222.1268
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ilarity 99.3%;
Conservative
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/note= '
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                    This Caby Clone, designated current in the Trom in man gene whose mutated form is associated with hereditary haemochromatosis whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmid-based corn library following identification of the HH locus in the HLA region of chromosome 6. A single mutation (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises chromosomes and in 4% to unaffected chromosomes. It results in a cys to Tyr substitution in the encoded protein (see AAW36499) at a cys to Tyr substitution in the encoded protein (see AAW36499) at a cys to Tyr substitution in the encoded protein (see AAW36499) at a cys to Tyr substitution in the encoded protein (see AAW36499) at a cys to Tyr substitution in the encoded protein (see AAW36499) at a cys to Tyr substitution in the encoded protein (Bee AAW36499) at a cys to Tyr substitution in the encoded protein (Bee AAW36499) at a cys to Tyr substitution in the HH gene product, its variants (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method testion an animal model for the HH disease; metal common HH gene mutation; an animal model for the HH disease; in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidation with HH disease; an antisense oligonucleotide directed against a transcriptional therapeutic agents for activity in commercion with HH disease; an antisense oligonucleotide directed against a transcriptional cor pairs of oligonucleotide sof the HH disea
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                                                                                                                                                                                                                                                                                                                                                                             This cDNA clone, designated cDNA24, is derived from human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 150; DB 18; Length 1440;
Pred. No. 1.6e-39;
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                                                                                                                                                                                              Thomas WJ;
                                                                                                                                                                                                                                                                                            Hereditary haemochromatosis gene and variants - usefu
and treatment of hereditary haemochromatosis disease
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                                                                                                                                                                                                Ruddy D,
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                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 4; 115pp; English.
                                                                                                                                                                                              Feder JN, Gnirke A,
Z, Wolff RK;
                                                                                                                                                             (MERC-) MERCATOR GENETICS INC.
                                                                                            96US-0652265.
96US-0630912.
96US-0632673.
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                                                                                                                                                                                                                                                             P-PSDB; AAW36499.
                                                                                                                                                                                                            Fsuchihashi Z,
                                                                                                23-MAY-1996;
 WO9738137-A1
                                                               04-APR-1997;
                                                                                                               04-APR-1996;
16-APR-1996;
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                                16-OCT-1997
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981 AAAGACGIATIGCCCAAIGGGGAIGGGACCIACCAGGGCIGGAIAACCIIGGGIGTACCC 1040
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                                                                                                                                                                                            HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss
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                                                                                                                                                Human hereditary hemochromatosis cDNA.
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AAC68429 standard; DNA; 1440 BP
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96US-0632673.
96US-0652265.
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Wolff RK;

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products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 150; DB 22; Length 1440; Pred. No. 1.6e-39; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                              Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1440 BP; 347 A; 354 C; 408 G; 331 T; 0 other;
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Best Local Similarity 99.3%;
Matches 150; Conservative
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16-APR-1996;
23-MAY-1996;
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                                       04-APR-1997;
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23-MAY-1996;
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31-OCT-2000
                                                                                                                                                                                                 Thomas WJ,
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    Human hereditary hemochromatosis 24d1 mutation cDNA.
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                                           HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 108pp; English.
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                                                                                                                                                                                                                                                        96US-0630912.
96US-0632673.
96US-0652265.
                                                                                                                                                                                                                     97US-0834497
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                                                                                                                                                                                                                                                                                                                                        (BIRA ) BIO-RAD LAB INC.
                                                                                                                                                                                                                                                                                                                                                                               Thomas WJ, Drayna DT,
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                                                                                                                                                                                                                       04-APR-1997;
                                                                                                                                                                                                                                                              04-APR-1996;
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23-MAY-1996;
                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                      Feder JN;
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RESULT 8 AAC68431

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P-PSDB; AAB19149.
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/product= "histocompatibility iron loading (HFE) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a 1-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequence encoding a histocompatibility iron loading (HFE) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                   Wolff RK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                       New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·,
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"if this base is mutated to C, then the
protein contains the mutation G93R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     99.3%; Score 150; DB 22; Length 1440; 99.3%; Pred. No. 1.6e-39; ive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; histocompatibility iron loading protein; HFE protein; major histocompatibility complex; non-classical class I gene; chromosome 6p; iron disorder; haemochromatosis; ss.
                      Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "if this base is mutated to G, protein contains the mutation
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"if this base is mutated to T,
----ing the mutation
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1440 BP; 348 A; 354 C; 407 G; 331 T; 0 other;
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                      Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                      Gnirke A,
                                                                                                                                                                                                          Disclosure; Fig 4; 108pp; English
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                      Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
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                                                                               WPI; 2001-006341/01
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Matches 150; Conserv
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                      Thomas WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA96769;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a human histocompatibility iron loading (HFE) protein. The HFE gene is a major histocompatibility (MFC) non-classical class I gene located or chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number 166119). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          700 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCAAGGAGTTCGAACCT
/*tag= f /*tag= f /*tag= f /*tag= f /*tag= f /*tag= lif this base is mutated to C, then the protein contains the mutation I105T, which is associated with an iron overload disorder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g. haemochromatosis, or a genetic susceptibility to develop it
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Pred. No. 1.9e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          BILL-) BILLUPS-ROTHENBERG INC
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Best Local Similarity 99.3%;
Matches 150; Conservative
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28-JUN-2000;
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                                                                           Homo sapiens.
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23-AUG-2000;
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                                                                                                                                    02-AUG-2001
This sequence represents the haemochromatosis (HC) gene. Mutations in this sequence are detected using the method of the invention. The method is for identifying an individual with hereditary haemochromatosis (HH) or a predisposition to develop HH or to genetically pass on HH to an offspring, comprising isolating a biological sample and amplifying a region of genomic DNA in the biological sample encompassing all or part of the DNA between markers D6S265 and D6S276, and detecting at least one homozygous or heterozygous mutation in a nucleotide within the region. The method can also be used for identifying an individual with an cutosomal recessive disorder (ARD) or predisposition to develop and/or genetically pass on an ARD to an offspring, comprises isolating a biological sample from the individual and screening genomic DNA in the sample for the presence of a homozygous or heterozygous (carriers) for the disorder. The method(s) can be used to identify individuals that are homozygous or heterozygous (carriers) for the mutation in a can be used to didentify individuals that are homozygous or heterozygous (carriers) for the mutation causing the ARD. Especially the method is used to diagnose HH or predisposition to HH by detecting a Cya282Tyr substitution. Individuals homozygous for this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic, immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                            Detection of autosomal recessive disorder - particularly hereditary haemochromatosis, by detecting a mutation in the HC gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.3%; Score 150; DB 19; Length 2727;
99.3%; Pred. No. 2e-39;
iive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;
                                                                                                                                                                                  Cullen LM, Jazwinska EC, Powell LW;
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                                                                                                                                                      (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                          Disclosure; Page -; 32pp; English.
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                                                                              97WO-AU00539
                                                                                                            96AU-0002083
                                                                                                                         96AU-0001849
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                                                                                                            03-SEP-1996;
23-AUG-1996;
                                                                               22-AUG-1997;
                                                                                                                                                                                       Busfield F,
                    WO9807884-A1
                                                   26-FEB-1998
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Matches
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vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
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2000US-0225214.
2000US-0222866.
2000US-0225267.
2000US-0225268.
2000US-0225268.
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2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0205515.
2000US-0209467.
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2000US-0224518.
2000US-0224519.
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2000US-0232080
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2000US-0231413
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2000US-0216647.
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2000US-0246528.
2000US-0246692.
2000US-0246693.
2000US-0246610.
2000US-0246613.
2000US-0246613.
2000US-0249207.
2000US-0249210.
2000US-0249211.
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2000US-0249218.
2000US-0249218.
2000US-0249218.
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2000US-0239937.
2000US-0241221.
2000US-0241786.
2000US-0241786.
2000US-024186.
2000US-0241809.
2000US-0241809.
2000US-0241809.
2000US-024617.
2000US-0246474.
2000US-0246476.
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2000US-0235834.
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2000US-0250160.
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2000US-0249265.
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01-DEC-2000;
01-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
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29-SEP-2000;
29-SEP-2000;
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20-OCT-2000;
20-OCT-2000;
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17-NOV-2000;
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13-OCT-2000;
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                                            27-SEP-2000;
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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human crissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, cher cancers of the adlesse, allergies, autoimmune hamolytic disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroidities, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; conditions autoimmune thyroiditis, diabetes mellitus, Crohn's disease, and (f) infectious diseases such as myocardial ischaemias; (d) wound parasitic infections.

Constant of infections diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.WiPO int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1748 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACC 1807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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                                                                                                                                                                                                                         Isolated polypeptide for treating, preventing and or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
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                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 3112; 781pp + Sequence Listing; English.
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                                                                                                                                           Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.3%;
Best Local Similarity 99.3%;
Matches 150; Conservative
                                                                                            (HUMA-) HUMAN GENOME SCI INC.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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                                                                                                                                           Barash SC,
                                                                                                                                                                                         WPI; 2001-451937/48.
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                                                                                                                                           Rosen CA,
                                                                                                                                                                                                                                                                                                            diagnosis
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Barash SC;

Rosen CA, Ruben SM,

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keratinocyte growth, hair loss, melanocyte growth, cell proliferation, cell growth, organ transplant; cell differentiation; body height; weight, hair colour; eye colour; skin, percentage of adipose tissue, pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; endocrine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content; carbohydrate content; vitamin content; cofactor content;
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2000US-225270P. 2000US-225447P. 2000US-225757P. 20000S-228924P 20000S-229343P 20000S-229344P 20000S-229345P 20000S-229345P 20000S-229513P 20000S-231413P 20000S-231413P 20000S-23423P 2000US-217496P. 2000US-218290P. 2000US-220963P. 2000US-234997P. 2000US-235834P. 2000US-236327P. 2000US-236367P. 2000US-239935P. 2000US-240960P. 2000US-241785P. 2000US-217487P. 000US-224518P 000US-224519P 0000US-225267P 000US-225758P. :000US-226868P 2000US-236368P. 2000US-236369P. 000US-237037P 17-JAN-2001; 2001US-0764877 2000US-236370P 2000US-236802P 000US-237038P 2000US-237039P 0000US-237040P 08-DEC-2000; 2000US-251869P nutritional component. US2002147140-A1 13-OCT-2000; 20-OCT-2000; 20-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; Homo sapiens. 08-SEP-2000; 21-SEP-2000; 14-AUG-2000; 01-SEP-2000; 05-SEP-2000; 25-SEP-2000; 29-SEP-2000; 02-OCT-2000; 14-AUG-2000; 10-OCT-2002

ROSEN C A. RUBEN S M. BARASH S C.

RUBE/)
BARA/) (ROSE/)

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The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metabatases, in animals or human. The nucleic acid: srimulates re-vascularisation of isohaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries.

CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and ALDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue continuous probably and adding strate and prometry stimulating keratinocyte growth; prevents kin aging due to sumburn by stimulating keratinocyte growth; prevents hair loss; since FGF family members activate hair-forming cells and promotes melanocyte growth, members activate hair-forming cells and promotes melanocyte growth, members activate hair-forming cells and promotes melanocyte growth, companient of merodecement of primary or grapes before transplantation of for supporting cells and bone marrow cells when used in combination with other cytokines; maintains or grapes before transplantation of mesodermal origin to differentiate of primary or grapes promote melance for pair, colour, skin, percentage of adipose tissue of pignentation, size, and shape (e.g., cosmetic surgery) involutes mammalian metabolism; changes mammalian sentel state or physical state by influencing blorthyms, creproductive capabilities, hormonal or endocrine levels, appetite, creproductive capabilities, hormonal or endocrine levels, appetite, creproductive capabilities, hormonal or endocrine levels, appetite, content, lipid, protein, carbohydrate, vitamins, mineral system antigen.

Note for the support of
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                                                                                       Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      printed specification, but was obtained in electronic format directly
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                                                                                                                                                                Disclosure; SEQ ID NO 3112; 321pp; English.
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                                           WPI; 2003-128199/12.
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Hereditary haemochromatosis gene and variants - useful for diagnosis
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"G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
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"C to G substitution (24d2 mutation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       results in His to Asp substitution'
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"A to T substitution (24d7 variant)
Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomas WJ;
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/note= "contains introns"
                                                                                                         Location/Qualifiers
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96US-0632673.
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Isuchihashi Z, Wolff RK;
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                                                                Homo sapiens
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16-APR-1996;
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It results in a cys to Tyr substitution in the encoded protein (see AAM36499) at a critical disulphide bridge important for secondary structure. The following are claimed: the HH genomic DNA [1], a 1437 bp CDNA sequence [1a] (see AAT96691) and their 24d1, 24d2 and 24d7 variants; a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants captide product chosen from the HH gene product, its variants (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method to determine the presence or absence of the common HH gene mutation; an animal model for the HH disease; metal chelation capents. T-cell differentiation factors and therapeutic agents for the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of inconverload; a method for screening potential. Cherapeutic agents for activity in connection with HH disease; an antisense oligonucleotide directed against a transcriptional product of a nucleic acid sequence as above; and oligonucleotides covering a range of nucleotides from (1), (1a) or their variants, useful for detecting a polymorphism in the HH gene. The invention also relates to methods for screening and the invention also relates to methods for screening and the invention also relates to methods for screening and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wolff RK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10825;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;
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Pred. No. 2.9e-39;
0; Mismatches 1;
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96US-0632673.
96US-0652265.
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Local Similarity 99.3%;
New 150; Conservative
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WPI; 2001-006341/01

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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                 New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.3%; Pred. No. 2.9e-39;
Matches 150; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;
                                                                                                                                                                    Disclosure; Fig 3; 108pp; English.
                           P-PSDB; AAB36869
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5809 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 5839 CCTGGGGAAGAGCAGATATACGTNCCAGG 151

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Search completed: February 11, 2004, 18:33:15 Job time : 112.113 secs

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1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCAATGCAATGCCAAGGAGTTCGAACCT

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
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Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 77, Appl
Sequence 1, Appli
Sequence 3112, Ap
Sequence 3112, Ap
GENERAL INFORMA
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Sequence 9, Appli
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Sequence 21, Appl
                                                                                                          February 11, 2004, 19:15:47; Search time 130.344 Seconds (without alignments) 4267.378 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpna/US06_PUBFW_PUB.seq:*

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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-138-888-10
US-10-138-888-10
US-10-138-888-11
US-10-138-888-12
US-10-138-888-12
US-10-138-888-12
US-10-242-515-3112
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US-10-138-888-1
US-10-138-888-5
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Maximum Match 100%
Listing first 45 summaries
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18770, Ap
4821, Ap
32571, A
2302, Ap
563, App
563, Appl
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Sequence 17,
Sequence 10
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Sequence
Sequence
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Sequence 3
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                                                                                                      Sequence
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-MAY-2002
CLASSIFICATION: CURKNOWN>
3. US-09-981-606-27

5. US-10-301-844-1

10-10-301-844-1

20-10-301-844-1

3. US-10-272-665-113

3. US-10-273-321-113

3. US-10-273-321-113

3. US-10-273-256-113

3. US-10-273-256-113

3. US-10-273-256-113

3. US-10-273-256-113

3. US-10-273-228-113

3. US-10-273-228-113

3. US-10-273-228-113

3. US-10-273-228-113

3. US-10-273-228-113

3. US-10-273-286-11044

3. US-10-128-057-346

2. US-10-128-057-346

3. US-10-128-057-347

3. US-10-128-995-32571

3. US-10-029-386-5014

3. US-10-128-057-351

2. US-10-128-057-381

3. US-10-29-386-5014

3. US-10-28-386-5014

3. US-10-28-386-5014

3. US-10-28-386-5014

3. US-10-28-386-5014

3. US-10-28-386-19081

US-09-964-761-21544
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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label= 24d1
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                                                                                                                                                                                                                                                                                                                                                     /note= "normal or wild-type (unaffected)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:

NAME/KEY: allele
LOCATION: replace(328, "g")

OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 150; DB 13; Length 517; Pred. No. 1.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   genomic sequence surrounding variant for A241(G) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (SEQ ID NO:1)"
                                                                               8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOCAGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                         TELECOMOUNICATION INFORMATION:
TELEPHONE: (312) 790-9090
TELEPHONE: (312) 699-8644
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
                                                        REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Peder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10138888 Publication No. US20030148972A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
    04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CCTGGGGAAGAGCAGAGATATACG
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                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                        NAME: Brian M. Poissant
FILING DATE: 04-APR-19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 150; Conservative
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                              FEATURE
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183 AACATCACCATGAAGTGGCTGAAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: 1.517
OTHER INFORMATION: /note= "genomic sequence surrounding variant for 24d1(A) allele corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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Pred. No. 1.8e-41;
0; Mismatches 1; Indels (
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-WAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGG 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence containing the HH gene
(SEQ ID NO:3)"
                                                                        APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: replace(328, "a")
OTHER INFORMATION: /phenoty7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864
INPORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CCTGGGGAAGAGCAGAGATATACGÍNC
                                                                                                FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 ceredecaacaacaaaararace
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Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brian M. Poissant
REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drayna, Dennis T.
Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gnirke, Andreas
Ruddy, David
                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.3
Matches 150; Conservative
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61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESONENCE ADDRESS:
RADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  PAPELICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
FILING DATE: 23-MAX-1996
APPLICATION NUMBER: US 08/632,655
FILING DATE: 13-MAX-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1155 Avenue of the Americas
                                                                                                                                     121 CCTGGGGAAGAGCAGAGATATAGGTNCRAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 790-9090
                                                                                                                                                                                                                                                                                            Sequence 10, Application US/10138888
Publication No. US20030148972A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
222..1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MCLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: replace(1066, "g")
OCHER INVERMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /phenotype= "normal or wild-type
                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: OF APELICATION NUMBER: US 08/634,497

RILING DATE: 04-APR-1997

APPLICATION NUMBER: US 08/652,265

FILING DATE: 14-APR-1996

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:
                            Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brian M. Poissant
REGISTATION UNDRER: 28,462
REFERENCE/DOCKET UNDRER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                               STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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LOCATION: replace(414, "a")
OTHER INFORMATION: /phenoty/
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-90
TELEFAX: (212) 869-8864
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LOCATION: 222..1268
           reuchihashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                          STATE: New York
                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (unaffected)"
/label= 24d2
                                                                                                                                                                                                                COUNTRY: USA
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/label= 24d1

1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT

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981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                                                                                                                                                                                                                                                                                                                                                             1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                               /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                     Length 1440;
                                                                                                                                                                                                                                                                                                                1; Indels
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COMPUTER: IBM PC Compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wolff, Roger K. TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                   Score 150; DB 13;
Pred. No. 2.4e-41;
0; Mismatches 1;
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REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
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STREET: 1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
APPLICATION NUMBER: US 08/632,673
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APPLICATION NUMBER: US 08/630,912
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-138-888-12; Sequence 12, Application US/10138888; Publication No. US20030148972A1; GENERAL INPORMATION:
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                                                                                                            LOCATION: replace (408, OTHER INFORMATION: /ph
                     CDS
222..1268
                                                                                                                                                                                                                                                                     99.3%;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                    NAME/KEY:
FEATURE:
NAME/KEY:
                                            LOCATION:
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                                                                  FEATURE
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                                                                                                                                                           1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                 Gaps
                                                                                                              0;
                                                                  Score 150; DB 13; Length 1440;
Pred. No. 2.4e-41;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wolff, Roger K.
INVENTION: Hereditary Hemochromatosis Gene
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REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 13-APY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
RAPPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
ATTORNEY/AGENT INFORMATION:
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                          121 CCTGGGGAAGAGCAGAGATATACGINCCAGG 151
       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-138-888-11; Sequence 11, Application US/10138888; Publication No. US20030148972A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        869-8864
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                                                                      99.3%;
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NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
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ZIP: 10036-2711
COMPUTER READABLE FORM:
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                                                                    Query Match
Best Local Similarity 99.3
Matches 150; Conservative
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US-10-138-888-10
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1041 ceresesaaseaseasararacerecease 1071
                           APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/52,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/53,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/530,912
FILING DATE: 04-APR-1996
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OTHER INFORMATION: /phenotyy
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                PRIOR APPLICATION DATA:
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
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LOCATION:
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LENGTH: 2506
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                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                             LOCATION: replace(408, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.3%; Score 150; DB 13; Length 1440; 99.3%; Pred. No. 2.4e-41; rive 0; Mismatches 1; Indels 0;
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
TRUChihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 77, Application US/10138888 Publication No. US20030148972A1 GENERAL INFORMATION:
                                                                                 LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 222..1268
                                                                                                                                                                                                                                                                                          NAME/KEY: allele
                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           label= 24d2
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61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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TITLE OF INVENTION: Mutations associated with iron disorders
FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
ATTORNEY AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LANGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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1688 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 1747
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PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR PLILING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-11
PRIOR PELING DATE: 2000-08-14
PRIOR PELING DATE: 2000-08-14
PRIOR PELING DATE: 2000-08-14
PRIOR PELING DATE: 2000-07-16
PRIOR PELING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-11
PRIOR PELING DATE: 2000-08-14
PRIOR PELING DATE: 2000-07-14
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Pred. No. 3.4e-41;
0; Mismatches 1; Indels 0
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Gnirke, Andreas
Ruddy, David
Tsuchashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/138,888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-10-138-888-1
; GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
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Best Local Similarity 99.3%;
Matches 150; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature LOCATION: (1222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-242-515-3112
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3112
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                                                                                                            1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                       700 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PC005
; CURRENT FILING DATE: 2001-01-17
; Prior application date removed - refer to PALM or file wrapper; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3112
LENGTH: 5749
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     99.3%; Score 150; DB 13; Length 2506;
99.3%; Pred. No. 2.7e-41;
ive 0; Mismatches 1; Indels 0
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99.3%; Pred. No. 3.4e-41;
tive 0; Mismatches 1; Indels 0
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PCOOSCI.
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
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CTHER INFORMATION: n equals a,t,g, or c
US-09-764-877-3112
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Publication No. US20040009488A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,629
PRIOR FILING DATE: 2000-02-04
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Best Local Similarity 99.33
Matches 150; Conservative
                             Best Local Similarity 99.3
Matches 150; Conservative
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ORGANISM: Homo sapiens
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US-09-764-877-3112
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NAME/KEY: SITE
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     Query Match
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"Hereditary Hemochromatosis (HH)
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REGISTRATION NUMBER: 28.462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccreegaagagcagagararacgraccage 5839
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APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
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                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HH) protein containing the 24d1 mutation"
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-10-138-888-5
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 869-8864
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                                                                                                                                                                                        NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE NOWER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPAR: (212) 790-9090
TELEPAR: (212) 869-8864
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                          (HH) protein"
/note= "No. US20030148972A1mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
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Pred. No. 4e-41;
0; Mismatches 1; Indels 0;
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OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
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Ruddy, David
Tsuchinashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5809 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 5839
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                    FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
                                                                              APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/834,497
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LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotyp
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Drayna, Dennis T.
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
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APPLICANT: Thoma
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99.3%; Score 150; DB 13; Length 10825;
Best Local Similarity 99.3%; Pred. No. 4e-41;
Matches 150; Conservative 0; Mismatches 1; Indels 0;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Feder, John N.
Gairke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
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NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 04-APR-1997

PILING DATE: 03-APR-1997

FILING DATE: 23-APR-1996

APPLICATION NUMBER: US 08/632,673
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                             COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5507..6023
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Best Local Similarity 99.3%;
Matches 150; Conservative
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                                                                                                             STATE: New York
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LOCATION:
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US-10-138-888-79
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                                                                                  COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFCATION PATA:
PRIOR APPLICATION DATA:
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Feder, John N.
Gnirke, Andreas
Ruddy, David
TBuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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gene 24d2 allele"
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REPERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/622,265
FILING DATE: 23-MAX-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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LOCATION: 5507..6023
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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GENBRAL INFORMATION:
APPLICANT: Thomas, Winston J.
Pravna, Dennis T.
                                                                  STATE: New York
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LOCATION:
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US-10-138-888-7
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELEPONMUNICATION INFORMATION:
TELEPRONE: (212) 790-9090
TELEPAX: (212) 869-8864
OTHER INFORMATION: /product= "Hereditar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Hereditary Hemochromatosis (HH) gene containing a combination of both 24d1 and 24d2 alleles"
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5749 AAAGACGTATTGCCCAATGGGGATGGGGACCTACCAGGCTGGATAACCTTGGCTGTACCC 5808
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LOCATION: replace(3878, "t")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing the 24d7 mutation" /note= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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99.3%; Score 150; DB 13; Length 10825;
Best Local Similarity 99.3%; Pred. No. 4e-41;
Matches 150; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                     COMPUTER: 1155 Avenue of the Americas
STREET: 1103A
ZIP: 10036-2711
COMPUTER: READAILE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ParentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION NUMBER: US 08/834,497
PRIOR APPLICATION NUMBER: US 08/834,497
            APPLICAN: Thomas, Winston J.
APPLICAN: Thomas, Dennis T.
Feder, John N.
Gnirk, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 28, 462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
FILING DATE: 04-APR-1996
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SEQUENCE DESCRIPTION: SEQ ID NO: 79:
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TELEFAX: (212) 869-8864
OTHER INFORMATION: /produ
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NAME: Brian M. Poissant
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GENERAL INFORMATION:
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5809 CCTGGGGAAGAGCAGATATACGTGCCAGG 5839
121 CCTGGGGAAGAGCAGAGATATACGINCCAGG 151
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Sequence 5, Al
Sequence 7, Al
Sequence 27, A
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Sequence 20
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Sequence 5
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ZIP: 45202-2917

COMPUTEY: USA

ZIP: 45202-2917

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: Diskette

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                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rundell, Clark A.
APPLICANT: Vary, Calvin P.H.
TITLE OF INVENTION: STABLE ENCAPSULTATED REFERENCE
TITLE OF INVENTION: NUCLEIC ACID AND METHOD OF MAKING
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wood, Herron & Evans, L.L.P.
US-08-652-265-7

US-08-834-497A-1

US-08-834-497A-3

US-08-834-497A-3

US-08-834-497A-7

US-09-503-444A-1

US-09-503-444A-3

US-09-503-444A-7

US-09-503-444A-7

US-09-577-454-7

US-09-679-729-27

US-08-724-394A-21

US-08-914-372C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2700 Carew Tower CITY: Cincinnati STATE: OH
                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-08-905-124-5
; Sequence 5, Application US/08905124
; Patent No. 6074825
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nucleic acid
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STRANDEDNESS: single
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 ORIGINAL SOURCE:
ORGANISM: hum
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                                                                                                    February 11, 2004, 15:39:52; Search time 27.4222 Seconds (without alignments) 2430.473 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-08-652-265-21
US-08-652-265-21
US-08-834-497A-21
US-09-503-444A-21
US-08-652-265-10
US-08-652-265-11
US-08-652-265-12
US-08-652-265-12
US-08-652-265-12
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US-08-834-497A-10
US-08-834-497A-11
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US-08-834-497A-11
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US-08-652-265-5
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                                                                                                                                                                                                                                                                             569978 seqs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                    09981606-1B_COPY_700_850
                                                                                                                                                                                                                              IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued Patents NA:*
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Match Length
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Perfect score:
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                                                                                                          Run on:
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183 AACAICACCAIGAAGIGGCIGAAGGAIAAGCAGCCAAIGGAIGCCAAGGAGIICGAACCI 242
                                                                         243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGCTGGATAACCTTGGCTGTACCC 302
                                        61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                                                                                                                  121 CCTGGGGAAGAGCAGAGATATACGINCCAGG 151
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APPLICANT: TBUChi
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US-08-632-673B-4
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US-08-632-673B-4
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STATE:
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                                                                                                                                      114 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 173
                                                                                                   1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
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                      Score 150; DB 3; Length 360;
Pred. No. 1.6e-43;
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                             234 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 264
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                                            Pred. No. 1.60
0; Mismatches
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APPLICATION NUMBER: US/08/632,673B
FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Embarcadero Center, CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08632673B Patent No. 5712098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 0179:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2402
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Drayna, Dennis T.
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Feder, John N.
TITLE OF INVENTION: HEREDITARY
TITLE OF INVENTION: DIAGNOSTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsuchihashi, Zenta
Gnirke, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Winston J.
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99.3%;
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 99.33
Matches 150; Conservative
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                                        Best Local Similarity 99.3
Matches 150; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-632-673B-3
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                          Query Match
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61 AAAGACGIAIIGCCCAAIGGGAIGGGACCIACCAGGGCIGGAIAACCIIGGCIGIACCC 120
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                                                                                               APPLICANT: Gnirke, Andreas
APPLICANT: Thomas, Winston J.
APPLICANT: Dromas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Wolff, Roger K.
APPLICANT: Welff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS
TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
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Pred. No. 1.8e-43;
0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,673B
FILIMS DATE: 16-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
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CITY: San Francisco
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Sequence 4, Application US/08632673B Patent No. 5712098
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                            Tsuchihashi, Zenta
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TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 326-2400
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Best Local Similarity 99.3%;
Matches 150; Conservative
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT

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Patent No. 6025130 GENERAL INFORMATION:
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                                                                                                                                                                                      APPLICANT: Tsuchihashi, Zenta
APPLICANT: Thomas, Minston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Trayna, Dennis T.
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Broger K.
APPLICANT: Feder, John N.
TITLE OF INVENTION: HERBOITARY HEMOCHROMATOSIS
TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
NUMBER OF SEQUENCES: 13
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentln RC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FILING DATE: 16-APR-1996
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1.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TWONNSRND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
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APPLICATION.
FILING DATE: 16-AL.
FILING DATE: 16-AL.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET VUMBER: 017957-000410
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2401
TELEPHONE: (415) 326-2401
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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  303 CCTGGGGAAGACAGAGATATACGTACCAGG 333
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99.3%; Score 150; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 151; Conservative 0; Mismatches
                                                                                                                                    Sequence 13, Application US/08632673B Patent No. 5712098 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-CONT
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                                                                                                                        US-08-632-673B-13
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STATE: CA
COUNTRY:
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RESULT 5 US-08-652-265-20 ; Sequence 20, Application US/08652265

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61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AAAGACCTATTGCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "normal or wild-type (unaffected) genomic sequence surrounding variant for 2441(g) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (SEQ ID NO:1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.3%; Score 150; DB 3; Length 517; 99.3%; Pred. No. 1.8e-43; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /phenotype= "normal or wild-type (unaffected)" /label= 24d1
                                                                 APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
CORRESPONDENCE: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/652,265
CLASSIFICATION: 514
                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: replace (328, "g")
OTHER INFORMATION: /phenoty;
OTHER INFORMATION: (unaffect
Thomas, Winston J.
                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 99.3
Matches 150; Conservative
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LOCATION: 1..517
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
                          Drayna,
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                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                   303 CCTGGGGAAGAGAGATATACGTACCAGG 333
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NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                 Sequence 20, Application US/08834497A Parent No. 6140305
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: replace(328, "g")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 20 SEQUENCE CHARACTERISTICS: LENGTH: 517 base pairs TYPE: nucleic acid STRANDEDNESS: single.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650-493-5556
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LOCATION: 1..517
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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              ਨੇ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 AAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "genomic sequence surrounding
variant for 24d1(A) allele corresponding
to positions 5507-6023 of genomic
sequence containing the HH gene
(SEQ ID NO:3)"
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Sequence 21 Application US/08652265

Sequence 21 Application US/08652265

Patent No. 6025130

GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and m.
STRRET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZUP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPRING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: 130-223
ATORNEY/AGENT INFORMATION:
NAME: SMICH, William M.
REDERENCE/DOCKET NUMBER: 17957-000500
TELEFRANCE/DOCKET NUMBER: 17957-000500
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= 24d1
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; OTHER INFORMATION: /label= 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.33
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: -
LOCATION: 1..517
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                          US-08-652-265-21
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APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Truchihashi, Zenta
APPLICANT: TRUCHIF, ROGER K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie F "A-
STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "normal or wild-type (unaffected) genomic sequence surrounding variant for 2441(6) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (SEQ ID NO:1)"
                                                                                                                                                                                                                                                                                                                                                             COKKESPONDENCE ADDRESS:
COKKESPONDENCE ADDRESS:
COKKESET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CONTRY: USA
ZIP: 10036-281

ZIP: 10036-281

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
FILING DATE: 04-APR-1996
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243 AAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                                                           /note= "genomic sequence surrounding
variant for 24d1(A) allele corresponding
to positions 5507-6023 of genomic
sequence containing the HH gene
(SEQ ID NO:3)"
                                                                                                                                                                                                                                                                                                                                                                            /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
99.3%; Score 150; DB 3; Length 517;
Best Local Similarity 99.3%; Pred. No. 1.8e-43;
Matches 150; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/09503444A

Sequence 20, Application US/09503444A

Patent No. 6228594

GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.

APPLICANT: Feder, John N.

APPLICANT: Gairke, Andreas

APPLICANT: Gairke, Andreas

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ANDRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 cerecedadedecadadararaceraceded 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CCTGGGGAAGAGCAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/09/503,444A
14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,44
                                                                                                                                                                                                                                                                                                                                                                                                                            /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIORICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                         LOCATION: replace (328, "a")
OTHER INFORMATION: /phenotyn
OTHER INFORMATION: /label=:
                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                       LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    LOCATION: 1..517
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: allele
                                                                                                                                      CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-503-444A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-834-497A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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                                                                                                                                                                                                                                                                                           61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                                                                                                                                                                                                                                                                                                                    243 AAAGACGTATTGCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302
                                                                                                                                                                                                  1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                             Gaps
                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Brder, John N.
APPLICANT: Ruddy, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                               Length 517;
                                                                                                                                                             1; Indels
/phenotype= "normal or wild-type (unaffected)"
/label= 24dl
                                                                                                                 Score 150; DB 3;
Pred. No. 1.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
CIASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                 303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333
                                                                                                                                                                                                                                                                                                                                                                                     121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8907-0056-999
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
PILING DATE: 16-APR-1996
CLASSIFICATION BATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-834-497A-21; Sequence 21, Sequence 17, Setten No. 6140365; Patent No. 6140365; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Polseant, Brian M.
REGISTRATION NUMBER: 28,462
REPERENCE/DOCKET NUMBER: 890
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21:
                                                                                                               99.3%;
Best Local Similarity 99.3%;
Matches 150; Conservative C
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
      OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-834-497A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 04
CLASSIFICATION:
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NAME/KEY: -
LOCATION: 1..517
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-503-444A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-652-265-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 AAAGACGTATTGCCCAATGGGGATGGGGACCTACCAGGGCTGGATAACCTTGGCTGTAGCCTGGTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "normal or wild-type (unaffected) genomic sequence surrounding variant for 2441(g) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (SEQ ID NO:1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.3%; Score 150; DB 3; Length 517; Best Local Similarity 99.3%; Pred. No. 1.8e-43; Matches 150; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/09503444A

Patent No. 6228594

GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.

APPLICANT: Feder, John N.

APPLICANT: Gilfke, Andreas

APPLICANT: Gilfke, Andreas

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TILLE OF INVENTION: Hereditary Hemochromatosis Gene

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /phenotype= "normal or wild-type
(unaffected)"
/label= 24d1
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STREET: 1155 Avenue of the Americas
                FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
APPLICATION NUMBER: 08/632,673
                                                                                                                       ATTORNAL PASSANT MANAGERIA MANE: POLSSANT, BRIAN M. REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
TELEX: 66141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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OTHER INFORMATION: (unaffecty
OTHER INFORMATION: (labele 2
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                                                                                  FILING DATE: 04-Apr-1996 ATTORNEY/AGENT INFORMATION:
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LOCATION:

COTHER INFORMATION:

OTHER INFORMATION:

OTHER INFORMATION:

OTHER INFORMATION:

OTHER INFORMATION:

OTHER INFORMATION:

PEATURE:

NAME/KEY: allele

LOCATION:

LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-503-444A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "genomic sequence surrounding variant for 24d1(A) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (SEQ ID NO:3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: allele
LOCATION: replace (328, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.3%; Score 150; DB 3; Length 517; 99.3%; Pred. No. 1.8e-43; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 ccresesaasasasasasararaksia 333
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                                                                                                                                                                                   FILING DATE: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/62,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORIEY/ABATI INFORMATION:
NAME: POISSANT INFORMATION:
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 212-790-9090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
PILLING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08652265 Patent No. 6025130
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APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.3
Matches 150; Conservative
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61 AAAGACGIATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 150; DB 3; Length 1440;
Pred. No. 2.7e-43;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                      GENERAL TROUGH WINSTON J.

APPLICANT: Drayna, Dennis T.

APPLICANT: Feder, John N.

APPLICANT: Guirke, Andreas

APPLICANT: Ruddy, David

APPLICANT: Ruddy, David

APPLICANT: Ruchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene

NUMBER OF SEQUENCES: 44

CORRESSEE: Townsend and Townsend and Crew LLP

ADDRESSEE: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTRE: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
                              1041 CCTGGGGAAGACAGAGATATACGTGCCAGG 1071
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121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                          Sequence 10, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1795
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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222..1268
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Best Local Similarity
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LOCATION: replace
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Ca
                                                                                                              RESULT 12
US-08-652-265-10
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99.3%; Score 150; DB 3; Length 1440;
Best Local Similarity 99.3%; Pred. No. 2.7e-43;
Matches 150; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /phenotype= "normal or wild-type
(unaffected)"
/label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /phenotype= "normal or wild-type
(unaffected)"
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(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING STSTEM: TC-LUCY MS-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILLING DATE: 23-MAY-1996
CLASSTETATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: SMILL, WIlliam M.
REGISTRATION NUMBER: 17957-000500
TELEBRACE/DOCKET NUMBER: 17957-000500
TELEBRACE ATTON INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INO: 9:
SEQUENCE (415) 576-0200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: LENGTH: linear
MOLECULE TYPE: CDNA
                                       APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               SSEE: Townsend and Townsend and Crew LLP
T: Two Embarcadero Center, Eighth Floor
San Francisco
: California
                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= 24d2
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CTHER INFORMATION: /phenotype:
CTHER INFORMATION: (unaffected);
CTHER INFORMATION: /label= ?^?
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OTHER INFORMATION: /phenotys
OTHER INFORMATION: (unaffect
OTHER INFORMATION: /label= 2
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OTHER INFORMATION: /phem:
OTHER INFORMATION: (unafi
OTHER INFORMATION: /label
FBAUURE: allele
                   Dennis T.
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222..1268
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                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                          STATE: Ca
                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                           CITY:
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g ਨੋ 1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071

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1041 CCTGGGGAAGAGCAGAGATATACGTACCAGG 1071

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LOCATION: replace(408, "g")
LOCATION: replace(408, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 24d2
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99.3%; Score 150; DB 3; Length 1440;
Best Local Similarity 99.3%; Pred. No. 2.7e-43;
Matches 150; Conservative 0; Mismatches 1; Indels
                                                                                                                       APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE MADDRESS:
ADDRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CCTGGGGAAGAGCAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: ...
FILING DATE: ...
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/COCKET VUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                            Sequence 11, Application US/08652265; Patent No. 6025130; GENERAL INFORMATION: APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222..1268
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RESULT 13
US-08-652-265-11
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61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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                                                                                                                                              APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Enbarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
99.3%; Score 150; DB 3;
Best Local Similarity 99.3%; Pred. No. 2.7e-43;
Matches 150; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 94111.3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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             Sequence 12, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUCCATION: replace (1066, "a")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: /label= 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: replace (408, "g")
OTHER INFORMATION: /phenotyn
OTHER INFORMATION: /label=:
                                                                                                          Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                            Feder, John N.
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EDNESS: single
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LOCATION: replace
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LOCATION:
FEATURE:
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JS-08-652-265-12
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Gaps .

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981 AAAGACGTATTGCCCAATGGGGATGGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040
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1; Indels
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Best Local Similarity 99.3%;
Matches 150; Conservative
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           APPLICANT: Thomas, Winston J.
APPLICANT: Trayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andraas
APPLICANT: Gnirke, Andraas
APPLICANT: Tsuddy, David
APPLICANT: Tsuddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: replace(408, "c")
OCHTER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION DATA:
APPLICATION DATE: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION S14
PRIOR APPLICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: US 08/630,912
FILING DATE: US 08-1996
CLASSIFICATION S14
ATTORNEY AGENT HYPORMATION:
AND ATTORNEY AND AND ATTORNEY AND ATTORNEY AGENT HYPORMATION:
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                                                                                                                                                                            1041 CCTGGGGAAGAGCAGAGATATACGTACCAGG 1071
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REGISTRATION NUMBER: 28,462
REFERENCE, DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPRAN: 650-493-4935
TELEPRA: 661-493-4935
TELERAM: 661-493-4935
TELERAM: 661-491-856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                           121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08834497A Patent No. 6140305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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222..1268
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LOCATION:
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US-08-834-497A-9
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Scoring table:

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Minimum DB Maximum DB

Database

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Sequence:

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K-EST0027329 S9SNU601 Homo sapiens cDNA clone S9SNU601-12-G03 5',
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fat: +82-42-860-44109
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: yongsung@mail.kribb.re.kr
Plate: 12 row: G column: 03
High quality sequence stop: 544.
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BM751283
BM751283.1 GI:19080901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
 102.6
102.6
102.6
102
102
98.8
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138.6
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136.8
123.1
121.4
119.2
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
BM751283
 AU279987 AU279987
CB162561 K-EST0223
BF883952 PM4-ET020
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                                                                  February 11, 2004, 14:16:30; Search time 1060.16 Seconds (without alignments) 6052.274 Million cell updates/sec
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        GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                       22781392 seqs, 12152238056 residues
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                              US-09-981-606-27_COPY_4652_4915
264
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Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
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9 AU279987
14 CB162561
10 BF883952
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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em_gss_inv:*
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gb_est4:*
gb_est5:*
em_estfun:*
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2: em_esthum:*
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5: em_estnu:*
6: em_estpu:*
7: em_estpu:*
7: em_estp1:*
10: gb_est2:*
11: gb_htc:*
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100.0
99.4
85.2
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Score

Result No.

264 264 262.4 225

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CB162561.1 GI:28148687
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JOURNAL
COMMENT
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/clone_lib="89SNU601"
/clone_lib="89SNU601"
/note="Organ: Stomach; Vector: pME18-FL3; Site_l: XhoI;
/note="Organ: Stomach; Vector: pME18-FL3; Site_l: XhoI;
Site_2: XhoI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Sfil site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Supersoript II using Sfil oligo-dT primer. After first strand synthesis, RNA was degraded by NoOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sil and cloned into DraIII - digested pME188-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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Imabayashi, H., Gojo,S., Kiyono,T., Sugiyama,T., Irie,R., Isogai,T., Mori,T., Hata,J., Tomoya,Y. and Umcawa,A.
Redifferentiation of dedifferentiated chondrocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with an expression profiling by large-scale cDNA analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GITCACACTCTCTGCACTACTCTTCATGGGTGCCTCAGAGGAGGACCTTTGGTCTTTTCCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 GCGGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
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Pred. No. 6.7e-73;
:: Mismatches 0;
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                                                                                                                               'tissue_type="Ascites"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 TGGAAAATCACAACCACAAGG 381
 Location/Qualifiers
                                                      /mol type="mRNA"
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Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: Maxamatsu,A.; Maxamatau,A.; Maxamatsu,A.; Ishii,S.; Yamamoto,J.; Isono
Y.; Saito,K.; Nakamura,Y.; Masuho,Y.; Nagai,K.; Isogai,T.
FAX: Maxama cDNA project; CDNA library construction & 5'-end one
Dass sequencing: Helix Research Institute.
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1 (Dases I to 535)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IGTITGAAGCTITGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Forea Research Institute of Bioscience & South Korea
Tel: +82-42-860-4470
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Pred. No. 6.8e-73;
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L17N670205n1-27-D07 5', mRNA sequence.
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100.0%; Pred. No. c.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="chondrocytes"
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143 c 168 g 124
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .560
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/clone="CHONS2002538"
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/Organizem: Trounc Bapticins
/mol type="mRNA"
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/dev_stage="Adult"
/clone lib="ET0209"
/note="Organ: lung tumor; Vector: puc18; Site 1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Parent application No. 196,716 - Indwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                Tel: +55-11-2704922

Pax: +55-11-2704922

Pax: +55-11-2707001

Pax: +55-11-2707001

Pax: +55-11-2707001

Pax: +55-11-2707001

Pax: +55-11-2707001

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-ET0209-151200-003-f07&t3=2000-12-15&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 17

High quality sequence start: 17

High quality sequence stop: 384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 TITICCAGTAGAATTITCAAGCCAGATGTGGCTGCAGCTGAGAGTCTGAAAGGGTGGG 207
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
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230846 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
87080089
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 225; DB 10;
Pred. No. 1.4e-60;
0; Mismatches 0;
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112 c 87 q 93 t
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/organism="Homo sapiens"
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/clone_lib="Li7N670205n1"
/clone_lib="Li7N670205n1"
/inche="Yogan: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F. Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
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PM4-ET0209-151200-003-f07 ET0209 Homo sapiens cDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 384)
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                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L17N670205n1-27-D07"
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                       /organism="Homo sapiens"
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: D column: 07
High quality sequence stop: 535.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TGGAAAATCACAACCACAGCAAGG 264
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                organism="Sus scrofa"
                                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 100 row: C column: 24
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 ACAACCACAACTACAGCAAG 414
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammala; Butheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 550) Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host="JH10B"
/clone_lib="WARC 2PIG"
/clone_lib="WARC 2PIG"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
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Pred. No. 1.1e-45;
0; Mismatches 51; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI339179 550 bp mRNA linear
364041 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BI339179
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 AAAATCACAACCACAGCAAG 263
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Tel: 402 762 4366

Fax: 402 762 4390

Fax: 402 762 4390

Banail: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

VO.9809044.e. Vector identified by cross_match with the -minscore 18

POR PRIMERS
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I (Dases 1 to 819)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 TGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 CACACTCCCTGCTCTTCTTCATGGGCGCCTCGGAGCCAGATCTCGGGCTGCCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 GTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="pooled"
/lab host="DH10B"
/lone lib="MARC 2PIG"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Ss Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta.
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80.4%; Pred. No. 1.2e-45;
ive 0; Mismatches 51; Indels
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'db xref="taxon:10090"
                                                                                                                                                                      'clone="IMAGE:652689"
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                                                                                                                                                                                                                                     dev_stage="4 weeks"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TGGAAAATCACAACCACAGCAAGG 264
                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J"
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Mus musculus
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                                                                                                                                                                                          sex="male"
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                                                        1. .464
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Best Local 9
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                                                                                                                                                                                                               /issue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC_15"
/clone_lib="NHH MGC_15"
/note="Corpus" colon; Vector: pOTB7; Site 1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
2 a 201 c 235 g 181 t
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mu89b05.rl Soares mouse lymph node NbMLN Mus musculus cDNA clone
IMAGE:652689 5' similar to TR:G940354 G940354 CLASS I
HISTOCOMPATIBILITY ANTIGEN-LIKE PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lalcy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 GACCAGCTGTTCGTGTTCTTATGATCATGAGAGTCGCCGTGTGGAGCCCCGGAACTCCATGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 GITTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGGTCAGAGTCTGAAAGGGTGG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GITTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGTGAGTCAGAGTCTGAAAGGGTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 GAICACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGGAAGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.4%; Score 178; DB 10; Length 819; 100.0%; Pred. No. 1.9e-45; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Possible reversed clone: similarity on wrong strand
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1711 row: d column: 06
                                                                                                                                    /organism="Homo sapiens"
                                                                  High quality sequence stop: 792
                                                                                                                                                                                                   clone="IMAGE:4857941"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                           Location/Qualifiers
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Fax: 314 286 1810
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Best Local Similarity
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3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Soares mouse lymph node NbMLN"
/note="Organ: lymph node; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 481)

Hayatau, T., Azakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
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'Y., Ito, M., Kawal, T., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Sakazume, N., Saski, D., Sato, K.,
Shibata, K., Shinagwa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
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RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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BB851691 RIKEN full-length enriched, B16 F10Y cells Mus musculus cDNA clone G370002P09 5', mRNA sequence.
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Seq primer: -28ml3 rev2 ET from Amersham. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 176; DB 9;
Pred. No. 6.2e-45;
0; Mismatches 55,
                                                                                                                                                                                                                                                                                                                                           'tissue_type="lymph node"
                                                                                                              organism="Mus musculus"
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BE994943
BE994943.1 GI:10678689
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'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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    .481
    /organism="Mus musculus"

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/clone="G370002P09"
                                Contact: Yoshihide Hayashizaki
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BE994943 11near EST 29-APR-2002 UI-M-CG0p-bik-d-03-0-UI-S1 NIH BMAP Ret4 S2 Mus musculus cDNA clone UI-M-CG0p-bik-d-03-0-UI 3', mRNA sequence.

DEFINITION

BE994943

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/clone lib="Will BMAP Ret4 52"
/clone lib="Will BMAP Ret4 52"
/note="Vector: pT7T3D-pac"(Pharmacia) with a modified
polylinker; Site l: Not I; Site 2: Eco Ri; The
NIH BMAP Ret4 52 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
TAG_SEQ=None found"
13 c 144 g 109 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine The following repetitive elements were found in this CDNA sequence: 1-31, >(CAG
                           Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Pred. No. 6.4e-45;
0; Mismatches 55; Indels
                                                                                                                     1 (bases 1 to 489)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                 Contact: Chin, H
National Institute of Mental Health
                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
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/strain="C57BL/6J"
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: M13 Forward POLYA=No.
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Fax: 301 443 9890
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Nuts musculus betazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 714)

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yadi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Quackenbush, J., Schrind, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bult, C., Hume, D.A., Coobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, J.L., Konasaya, A., Karadi, D., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaij, H., Kawaswa, Y., Kedzierski, R.M., King, B.L., Konasaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, H., Nagashima, T., Numata, K., Okido, T., Pavan, W., Jackson, I.J., Miki, P.A., Majlott, D.R., Maltais, L., Marchionni, L., Mckenzie, L., Miki, P.A., Magolima, T., Numata, K., Okido, T., Pavan, W.J., Pettea, G., Pettovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Red, J.C., Red, J.C., Red, J.C., Red, J.C., Rengisawa, R.D., Tangual, M., Sandellin, A., Schneider, C., Semple, C.A., Setou, R.D., Tomita, M., Varado, R., Winshaw-Boris, A., Yanagisawa, K., Sultana, R., Takenaka, Y., Taylor, M., Sahamada, K., Sultana, R., Takenaka, Y., Taylor, M., Sahamada, K., Sultana, E., Wunshaw-Boris, A., Yanagisawa, Carninci, P., Hayetsu, N., Hirozane-Kishikawa, T., Komo, H., Nakamura, M., Sakazume, N., Sakazume, N., Sakazume, N., Sakazume, N., Sakazume, N., Sabawi, D., Sabaki, S., Sabaki, S., Sabaki, D., Sabaki, S., Sabaki, S.
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243 ATCTGAGTCAGAGCCTGAAAGGTGGGACTACATGTTCATAGTAGACTTCTGGACCATCA 302
                                                                                                                                                                                                                                                                                                                                              BY747346 BIKEN full-length enriched, 2 days neonate thymus thymic cells (NOD) Mus musculus cDNA clone B430034J19 5', mRNA sequence.
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URL:http://genome_gsc.riken.go.jp,
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with
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Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                         303 regerararardecacacras
                                                                                                           241 TGGAAAATCACAACCACAGGAAGG 264
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TITLE

COMMENT

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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                               Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Fulloome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
genes. Genome Res. 10 (10), 1617-1630 (2000)
KIKRN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone="E430034719"
/tisque_type="thymic cells"
/clone_lib="RIKEN full-length enriched, 2 days neonate
thymes_thymic_cells (NOD)"
194 c 208 g 146 t
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Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430034J19

product:hemochromatosis, full insert sequence.
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Pred. No. 7.7e-45;
0; Mismatches 55; Indels (
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High-efficiency full-length cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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1. .714
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/strain="NOD"
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Best Local Similarity 79.2%;
Matches 209; Conservative 0
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MEDLINE PUBMED REFERENCE AUTHORS

JOURNAL

REFERENCE AUTHORS

JOURNAL MEDLINE PUBMED

TITLE

MEDLINE PUBMED

AUTHORS

REFERENCE

JOURNAL

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|db_xref="FANTOM DB:E430034J19"
|db_xref="taxon:10090"
|db_xref="taxon:10090"
|db_xref="taxon:10090"
|cell_type="thymic cells"
|tissue_type="thymus"
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VDFWTIMGNYNHSKVTKLGVVEWDEHKIRAKQNRDYLEKDCPEGLKRLLEIGRGYLGQOVP

TLVKVTRHWASTGGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVLPNGDETYG

GWLTLANAAPGDETRRTCQVBHPGLDPLTASWEPLGSGAMIIGIISGVTVCAIFLVGI

LFLILRKRKASGGTWGGYVLTDCE"
                                           Fax:81-45-503-9216)
CONA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                              prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Mospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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                  URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1719;
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                                                                                                                                                                                                                                                                                                                                                            assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
1..l719
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Pred. No. 1.2e-44;
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7. .1173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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/note="putative"
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                                                                                                                                                                                                                                                          genes
                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sagaki, N., Carninci, P., Konno, H., Aiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Zakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Grup, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1719)
                                                                                                                               Itoh, M., Konno, H., Okazaki, Y., Muramateu, M., Sugahara, Y., Shibata, K., Normalization and Bubraction of cap-trapper-selected cDNAB to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
Meth. Enzymol. 303, 19-44 (1999)
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TITLE JOURNAL MEDLINE PUBMED

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS

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TITLE JOURNAL

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/tissue_type="tongue"
/clone lib="RIKEN full-length enriched mouse cDNA library"
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99. 1178
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QGWLTLAVAPGDBTRFTCQVBHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVG
                                                                                                                                                                                                                                                                                            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Pax:81-45-503-9222,
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        Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,P., Ohno,M., Okazaki,Y., Okido,T., Oxazo,H., Saito,R., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.
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                                                                                                                                                                                                                                               Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="FANTOM_DB:2310032M04"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/protein_id="BAB26373.1"
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/db_xref="MGI:109191"
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                                   HTC 05-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramstsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. SHIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                           Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032M04 product:hemochromatosis, full insert
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/lab host="BH10B (Life Technologies)"
/clone lib="NH1 BMAP Ret4 S2"
/note="Vector: pT73D-Pec (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH BMAP Ret4 S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF465475 11 DEC-2000 TINEAR TINEAR BATCH DEC-2000 UI-M-CG0p-bqp-a-01-0-UI-BMAP Ret4_S2 Mus musculus cDNA clone UI-M-CG0p-bqp-a-01-0-UI 3', mRNA sequence.
TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
                                                                                        GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 392)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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|strain="C57BL/6J"
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Email: mEST@mail.nih.gov
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Sokaryota; Murinae; Mus. Sokaryota; Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kiyosawa, H., Yagi, K., Tomatu, Y., Halegamai, R., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hune, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matchad, H., Batalov, S., Belsel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.B., Cousins, S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Manai, Hir, Kawasawa, N., Jackson, J.J., Jarvis, B.D., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, Y. H., Maglott, D.R., Mallais, L., Marchionni, L., McKenzie, E., Miki, P. A., Maglott, D.R., Mallais, L., Pontius, J.U., Qi, D., Pertea, G., Petrovsky, M., Sahmada, K., Sultana, R., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Schneider, C., Semple, C.A., Wagnald, M., Sandelin, A., Schneider, C., Semple, C.A., Wagnard, M., Sakazume, N., Sakazume, N., Hayasu, J., Waki, K., Kawai, J., Marawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishia, Y., Janger, J., Manayasa, J., Manayasa, J., Waki, A., Sakai, J., Kawa, J., Manayasa, J., Hayasui, J., Waterston, R., Lander, M., Sakazume, N., Sakazume, N
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KEYWORDS
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence full-length cDNA encyclopedia: real-time sequence Justering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                         Denail: genome-resogno.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Alzawa,K., Akimura,T., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Kouno
H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Tissues were provided by David A. Hume ( Depts. of Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone_lib="RIKEN full-length enriched, bone marrow
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  Contact: Yoshihide Hayashizaki
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/strain="C57BL/6J"
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ALIGNMENTS

iron absorption regulator; intracellular iron absorption; lung injury; haemcchromatosis; transfusion; thalassaemia; haemolytic anaemia; chronic infection; transferrin receptor; TfR, brain tumour; cancer; oxidative stress disorder; tissue damage; vascular disease; inflammation, atherosclerosis; autoimmune disease; inflammatory condition; gene; ss. Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia; DNA encoding beta 2 microglobulin (beta2M)/HFE monochain. Location/Qualifiers BP ABK49917 standard; cDNA; 1317 (first entry) Homo sapiens 15-JUL-2002 ABK49917; Key

/*tag= a /product= "beta2M/HFE monochain" /*tag= WO200224929-A2

28-MAR-2002.

24-SEP-2001; 2001WO-US29873

AAT96691 standard; cDNA; 1440 BP.

AAT9669.

AAT96691;

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The invention relates to a soluble polypeptide (I) of beta 2

microglobulin (beta2m)/HFE monochain comprising human beta2m (or its

microglobulin (beta2m)/HFE monochain comprising human beta2m (or its

manalogue or active fragment), linked to alphal-alpha3 domains of human

HFE (a central regulator of iron absorption; undefined), or its analogue

or active fragment, by a flexible linker peptide, or a functional

Gerivative or salt of (I). (I) is useful for reducing intracellular iron

absorption in patients having hereditary haemochromatosis, transfersions,

thalassaemias, haemolytic anaemia or chronic infections, and for

construction are preferably lymphocytes or leukocytes, across the blood-

brain barrier. (I) is further useful for treating brain tumour. (I)

construction of treating oxidative stress disorders resulting in

tissue damage e.g. vascular diseases, inflammation, atherosclerosis,

cutoimmune diseases and inflammatory conditions. The monochain manifests

specific characteriatics advantageous for drug delivery systems. It is a

sutoimmune diseases and inflammatory conditions. The monochain manifests

cutoimmune diseases and inflammatory conditions. The monochain manifests

specific characteriatics advantageous for drug delivery systems. It is a

soluble, stable and fully conformed protein. It binds specifically to

transferriar receptor. If is continuously internalised by the target cells, thus

colls, minimising side effects. It negatively regulates iron absorption,

cells, minimising side effects. It negatively regulates iron absorption,

cells, minimising side effects of newsorp expensed to this receptor in the blood as is transferrin. It should not induce an

collium response since it is a self non-polymeric protein and delivery of

manner response since it is a self non-polymeric protein and delivery of

manner of manner manner manner manner manner is is a

coll manner manner manner manner manner manner is not diluted in the blood as is transferring the protein and delivery of

coll manner ma
                                                                                                                                                                                                                                                                           Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     natural TfR-binding protein. The present sequence represents the coding sequence of beta2m/HFB monochain.
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                                                    UNIV RAMOT APPLIED RES & IND DEV LTD.
                                                                                                                                                Laham N;
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 2; 77pp; English.
                                                                                                                                             Rotem-Yehudar R,
  22-SEP-2000; 2000US-234843P.
                                                                                                                                                                                               2002-383192/41
                                                                                     MCINNIS P
                                                                                                                                                                                                                                                                                                                                                                   a linker peptide
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                                                    (UYRA-)
(MCIN/)
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                                            Gaps
Query Match
100.0%; Score 264; DB 24; Length 1317;
Best Local Similarity 100.0%; Pred. No. 9.2e-77;
Matches 264; Conservative 0; Mismatches 0; Indels 0;
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This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmaid-based CDNA library following identification of the HH locus in the HLA region of chromosome 6. A single mutation (24d1) in the HH gene ppears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a chromosomes and in 4% of unaffected chromosomes. It results in a chromosomes and in 4% of unaffected chromosomes. It results in a critical disulphide bridge important for secondary structure. The following are claimed: a lose's by genomic DNA sequence (I) (see following are claimed: a lose's by genomic DNA sequence (I) (see following are claimed: a lose's by genomic by and their 24d1, 24d2 and 24d7 variants; a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these an antibody produced using the peptide; a method crodermine the presence or absence of the common HH gene mutation; an animal model for the HH disease; metal chelation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - useful for diagnosis
                                                                                                                                                                                                                                                                                                                                                                     i
"G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
                                                                                                                                                                                                                                           g
"C to G substitution (24d2 mutation)
results in His to Asp substitution"
                                                                                                                                                                                                                                                                                                     h
"A to T substitution (24d7 variant)
results in Ser to Cys substitution"
                                                                                            Hereditary haemochromatosis; metal toxicity; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hereditary haemochromatosis gene and variants - usefi
and treatment of hereditary haemochromatosis disease
                                                            Hereditary haemochromatosis gene cDNA clone.
                                                                                                              gene therapy; prenatal screening; human; ss.
                                                                                                                                                                           Location/Qualifiers
222.1268
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96US-0630912.
96US-0632673.
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Tsuchihashi Z, Wolff
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                                                                                                                                           Home sapiens.
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16-APR-1996;
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alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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       New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hereditary hemochromatosis gene products or polypeptides, useful
                                                                                         The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed shaving human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for
                                                                                                                                                                                                                               Length 1440;
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                                                                                                                                                                                               Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human hereditary hemochromatosis 24d1 mutation cDNA.
                                                                                                                                                                                                                            100.0%; Score 264; DB 22; 100.0%; Pred. No. 9.6e-77;
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                                                               Disclosure, Fig 4; 108pp; English.
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96US-0652265.
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16-APR-1996;
23-MAY-1996;
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agents, T-cell differentiation factors and therapeutic agents for the mitigation of injury due to oxidative process in vivo or mitigation of iron overload, a method for screening potential therapeutic agents for activity in connection with HH disease, an antisense oligomorleotide directed against a transcriptional product of a nucleic acid sequence as above, and oligomorleotides or pairs of oligomorleotides covering a range of nucleotides from (I), (Ia) or their variants, useful for detecting a polymorphism in the HH gene. The invention also relates to methods for screening for HH homozygotes, to HH diagnosis, prenatal screening and diagnosis, and therapies of HH disease, including gene therapy,
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                                                  The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cal differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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  treating hereditary hemochromatosis in a patient, and as a metal
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S65C"
                                                                                                                                               Query Match 100.0%; Score 264; DB 22; Length 1440; Best Local Similarity 100.0%; Pred. No. 9.6e-77; Matches 264; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequence encoding a histocompatibility iron loading (HFE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, histocompatibility iron loading protein, HFE protein, major histocompatibility complex; non-classical class I gene, chromosome 6p, iron disorder; haemochromatosis; ss.
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/*tag= a
/product= "histocompatibility iron loading
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                                                                                                                                                                                        GTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACC
                                                                                                                           Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;
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"if this base is mutated to C,
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           chelation agent alleviating iron overload
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                              Disclosure; Fig 4; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                               TGGAAATCACAACCACAGGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a human histocompatibility iron loading non-classical class I gene is a major histocompatibility (MHC) non-classical class I gene located chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number 160319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC
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"if this base is mutated to C, then the
protein contains the mutation I105T, which
is associated with an iron overload disorder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing an iron disorder e.g., hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutat in exon 2 or an intron of a histocompatibility iron loading nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BILL-) BILLUPS-ROTHENBERG INC
                                                                                                                                                                                                                                                                                                                                                                                                                99US-0277457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the haemochromatosis (HC) gene. Mutations in this sequence are detected using the method of the invention. The method is for identifying an individual with hereditary haemochromatosis (HH) or a predisposition to develop HH or to genetically pass on HH to an offspring, comprising isolating a biological sample and amplifying a region of genomic DNA in the biological sample encompassing all or part of the DNA between markers D65255 and D65276, and detecting at least one homozygous or heterozygous mutation in a nucleotide within the region. The method can also be used for identifying an individual with an autosomal recessive disorder (ARD) or predisposition to develop and/or genetically pass on an ARD to an offspring, comprises isolating a biological sample from the individual and screening genomic DNA in the sample for the presence of a homozygous or heterozygous mutation in a gene, the normal function of which, is required to prevent progression of the disorder. The method is can be used to identify individuals that are homozygous or heterozygous (carriers) for the mutation causing the ARD. Especially the method is used to diagnose HH or predisposition to HH by detecting a Cys282Tyr substitution. Individuals homozygous for this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                             Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of autosomal recessive disorder - particularly hereditary haemochromatosis, by detecting a mutation in the HC gene
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                                                                                                                                                                                                                                                                                                                                                                                                                  Powell LW;
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100.0%; Pred. No. 1.2e-76;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                  Jazwinska EC,
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                                                                                                                  autosomal recessive disorder; ss
                                                                                                                                                                                                                                                                          97WO-AU00539
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96AU-0001849
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Les 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Cullen LM,
                                                      Haemochromatosis gene
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                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                        22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                   23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                  Susfield F,
                  10-JUL-1998
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3582 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTTATTA 3641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon cancer, and diagnosing or monitoring the presence of metastases of colon cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3402 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to human colon specific nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; colon; cytostatic; vaccine; gene therapy; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5982 BP; 1659 A; 1247 C; 1518 G; 1556 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated colon-specific nucleic acid molecule, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                               Human colon specific nucleic acid, SEQ ID 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3642 TGGAAAATCACAACCACAGCAAGG 3665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 155-156; 216pp; English.
          561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu
TGGAAATCACCACAGCAAGG
                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon disorder; metastasis; ds.
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                                                                                                                                                                         ABV93934 standard; DNA; 5982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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3822 TGTTTGAAGCTTTGGGCTACGTGATGACCAGCTGTTCGTGTTCTATGATCATGAGGTC 3881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HLA region of chromosome 6. A physical clone coverage was then generated extending from D6S265, which is a marker that is centromeric of HLA-A, in a telomeric direction through D6S276, a marker at which cate all the allelic association was no longer observed. A single mutation (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a fto A substitution that is present in C6 4 affected chromosomes and in 44 of unaffected chromosomes. It results in a Cys to Tyr substitution in the encoded protein (see AAW36499) at a critical disulphide bridge important for secondary comparates, a cloning or expression vector; host cells, a structure. The following are claimed: the HH genomic DNA (1), a 1437 bp cDNA sequence (1a) (see AAT96691) and their 24d1, 24d2 and 24d7 variants; a cloning or expression vector; host cells; a comprise of these an antibody produced using the peptide; a method cesiques of these; an antibody produced using the peptide; a method cesiques of these; an antibody produced using the peptide; a method cesiques of these; an antibody produced using the peptide; a method cesiques of these; an antibody produced using the peptide; a method cesiques of the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to connection with HH disease; an antisense oligonucleotide directed against a transcriptional corpuses or pairs of oligonucleotide directed against a transcriptional corpuses or pairs of oligonucleotides covering a range of mucleotides covering and suppositing and therappeutics, and therappeutics, and therappeutics, and therappeutics, and therappeutics, and therappeutics, and therappeutics, and therappeutics, and therappeutics, and therappeuti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 100.0%; Score 264; DB 18; Length 10825; Local Similarity 100.0%; Pred. No. 2.2e-76; Los 264; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAAAATCACAACCACAGCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This genomic DNA sequence corresponds to the human gene whose mutated form is associated with hereditary haemochromatosis (HH)
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"G to A substitution (24d1 mutation
associated with HH), results in Cys to
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"C to G substitution (24d2 mutation)
results in His to Asp substitution"
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                                                                                                                                                                                                                                     Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.
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/note= "contains introns"
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361..7147
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                                                                                                                                                                                        Hereditary haemochromatosis gene.
                                                   AAT96690 standard; DNA; 10825 BP
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96US-0630912.
96US-0632673.
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Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                           137..3761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                   The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cap may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                         1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                          New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 264; DB 22; Length 10825; 100.0%; Pred. No. 2.2e-76; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                             Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human hereditary hemochromatosis 24d1 mutation DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds
                                                                                                                                               Gnirke A, Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAAATCACAACCACAGGAAGG 4025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264
                                                                                                                                                                                                                                                  Disclosure, Fig 3; 108pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
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                                                                                 96US-0630912.
                                                             97US-0834497
                                                                                             96US-0632673
                                                                                                      96US-0652265
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                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 264; Conservative
                                                                                                                         (BIRA ) BIO-RAD LAB INC
                                                                                                                                               Drayna DT,
                                                                                                                                                                            2001-006341/01
                                                                                                                                                                                     P-PSDB; AAB36869
                                                                                  04-APR-1996;
16-APR-1996;
 Homo sapiens
                                                             04-APR-1997;
                                                                                                      23-MAY-1996;
                    US6140305-A.
                                         31-OCT-2000
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                                                                                                                                             Thomas WJ,
                                                                                                                                                         Feder JN;
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3822 IdrirdaAgcrirdGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGGTC 3881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3762 Gricacacicicrecaciacercircareserecercaesecaeseceresesecenses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                       Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 264; DB 22; Length 10825; 100.0%; Pred. No. 2.2e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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major histocompatibility complex; non-classical class I gene;
chromosome 6p; iron disorder; haemochromatosis; ss.
                                                                                                                                                                                                                                                                                       Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic DNA of a histocompatibility iron loading (HFE) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                    Gnirke A, Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3; 108pp; English.
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                                                                                                         96US-0630912.
96US-0632673.
96US-0652265.
                                                       97US-0834497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264; Conservative
                                                                                                                                                                                                                                                                                 Thomas WJ, Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                         (BIRA ) BIO-RAD LAB
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-006341/01
                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAB36870.
                                                    04-APR-1997;
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16-APR-1996;
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31-OCT-2000
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AAV57926;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the human histocompatibility iron loading (HFE) gene. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number U60319). The presence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barton JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 21-28; 55pp; English.
                            location/Qualifiers
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/number= 6
10206..10637
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7995..9050
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4652..4915
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          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                  4772 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTTCAAGCCAGATGTGGCTGC 4831
                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                    181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine butyrophilin; BT; human hereditary haemochromatosis; HPE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupua; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss.
                                                                                                                                                                                                                                                        61 IGTITGAAGCTTTGGGCTACGTGCATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC
                                                                                                                                                                                                                                                                                                                              121 GCCGTGTGGAGCCCCGGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
                                                                                                                                                                                                                    1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an individual
mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder e.g. haemochromatosis, or a genetic susceptibility to develop it.
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
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                                                                                                          Length 12146;
                                                                                                                                              ·.
                                                                         0 other;
                                                                                                                                              Indels
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                                                                         2474 C; 2911 G; 3378 T;
                                                                                                          ch 100.0%; Score 264; DB 21; Il Similarity 100.0%; Pred. No. 2.3e-76; 264; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                         Sequence 12146 BP; 3383 A;
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i Z, Wolff RK;
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                                                                                                          Query Match
Best Local S:
Matches 264
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Wolff RK;

Tsuchihashi Z,

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unaffected by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFP) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of the haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFB gene mutation in the genome of the individual. The HFB gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present including all all and antagonists of BT function. Also described are: (1) a RoRet gene which can be used to develop products for the study, diagnosis and which are homologues of a type I sodium transport gene, and NPT4 genes which are homologues of a type I sodium transport gene, and can similarly be used for hypophosphatemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hereditary haemochromatosis subregion from an HH affected individual
                                                                                                                                                                                                                                                                                                                                                                                                       / Match 100.0%; Score 264; DB 19; Length 235033; Local Similarity 100.0%; Pred. No. 7.8e-76; les 264; Conservative 0; Mismatches 0; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                             Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;
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Thomas WJ;

Ruddy DA,

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products from the human haemochromatosis game. The present sequence represents a hereditary haemochromatosis game. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis (HFB) affected individual. Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFB gene mutation in the genome of the individual. The HFB gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFB. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a Roket gene and antagonists of sevence of a syndrome, and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can
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                                                                                    editary haemochromatosis gene products - used to develop products the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                          present invention describes hereditary haemochromatosis gene
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Wolff RK

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Tsuchihashi

Gnirke A, Ruddy D,

96US-0630912. 96US-0632673. 96US-0652265.

97US-0834497

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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                    New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                      Disclosure; Fig 4; 108pp; English.
                                                                                                                     (BIRA ) BIO-RAD LAB INC
                                                                                                                                                   Thomas WJ, Drayna DT,
                                                                                                                                                                                            WPI; 2001-006341/01.
                            04-APR-1997;
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                                                                                                                                                                 Tsuchihashi
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96US-0652265.
                                            97US-0834497.
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                                                                                                                                                                Thomas WJ, Drayna DT,
Feder JN;
                                                                                                                                                                                                             WPI; 2001-006341/01.
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Best Local Similarity
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23-MAY-1996;
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                                                                                                                                          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACC
                                          Score 262.4; DB 22; Length
Pred. No. 3.2e-76;
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                                              99.4%;
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Hes 263; Conservative
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Job time
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Human hereditary hemochromatosis 24d1/2 mutation cDNA

(first entry)

21-FEB-2001

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BP

AAC68432 standard; DNA; 1440

RESULT 15

HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss

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* Design

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Sequence 9, Appli Sequence 10, Appl Sequence 25, Appl GENERAL INFORMA GENERAL INFORMA SEQUENCE 27, Appl Sequence 1, Appli Sequence 11, Appli Sequence 11, Appl Sequence 11, Appl Sequence 12, Appli Sequence 12, Appli Sequence 17, Appl GENERAL INFORMA GENERAL INFORMA GENERAL INFORMA US-10-138-888-9 US-10-138-888-10 US-09-981-606-1 US-10-018-888-1 US-10-138-888-3 US-10-138-888-3 US-10-301-844-1 US-10-301-844-1 US-10-138-888-11 US-10-138-888-12 US-10-138-888-17 US-10-138-888-5 US-10-138-888-5 US-10-138-888-5 US-10-138-888-5 US-10-138-888-5 US-10-138-888-5 US-10-138-888-7 10825 10825 10825 12146 235033 237326 0.001 0.001 0.001 0.001 4.

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Sequence 105, App Sequence 110, App Sequence 110, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 13068, Sequence 13068, Sequence 13068, Sequence 13068, Sequence 13068, Sequence 104, App Sequence 104, App Sequence 201, Appl Sequence 20, Appl	
US-10-158-057-105 US-10-272-665-110 US-10-272-756-110 US-10-272-756-110 US-10-273-228-111 US-10-273-321-111 US-10-273-321-111 US-10-273-321-111 US-10-273-321-111 US-10-273-321-111 US-10-273-321-111 US-10-273-321-111 US-10-273-321-111 US-10-273-321-111 US-10-273-321-130689 US-10-27-632-130689 US-10-027-632-130689 US-10-027-632-130689 US-10-027-632-130689 US-10-027-632-130689 US-10-027-632-130689 US-10-027-632-130689 US-10-027-632-130689 US-10-027-632-130689 US-10-27-632-130689 US-10-27-632-130689 US-10-27-632-130689 US-10-28-88-21 US-10-28-88-206 US-10-28-88-206 US-10-29-386-206 US-10-29-386-206 US-10-29-386-206 US-10-27-632-209965 US-10-027-632-209965	ication US/10138888 US2030148972A1 TIONS: Thomas, Winston J. Drayna, Dennis T. Gnirke, Andreas Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Ruddy, David Wolff, Roger K. INVENTION: Hereditary Hemochromatosis Gene SEGUECE: 79 BENGES: 79 BENGES: 79 BENDESS: ESSEE: Pennie & Edmonds LLP ET: New York INEY Ponnie & Edmonds LLP ET: New York INEY Ponnie & Edmonds LLP READABLE FORM: UM TYPE: RIOPPY disk UM TYPE: RIOPPY disk UM TYPE: RIOPPY disk UM TYPE: RIOPPY disk ATING SYSTEM: PC-DOS/MS-DOS WARE: Patentin Release #1.0, Version #1.30 BPLICATION NUMBER: US 08/652,265 ICATION NUMBER: US 08/652,265 ICATION NUMBER: US 08/632,673 NG DATE: 16-ARR-1996 ICATION NUMBER: US 08/632,673 NG DATE: 16-ARR-1996 ICATION NUMBER: US 08/632,673
596 1000 1300 1000 1300 1000 1300 1000 13	ALIGNO 10. Application US/10138888 10. US20030148972A1 10. RALICANT: Thomas, Winston J. 10. Drayna, Dennis T. 10. Feder, John N. 10. Gnirke, Andreas 10. Ruddy, David 10. TITLE OF INVENTION: Hereditary H. 10. WOBER OF SEQUENCES: 79 10. CORRESPONDENCE ADDRESS: 10. ADDRESSEE: Pennie & Edmonds 10. STATE: New York 10. COMPUTER: 1155 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. COMPUTER: 1150 Avenue of the J. 10. FILING DATE: 02 App. 1997 10. APPLICATION NUMBER: US 08/6: 10. FILING DATE: 12-APR. 1996 10. APPLICATION NUMBER: US 08/6: 10. FILING DATE: 12-APR. 1996 10. APPLICATION NUMBER: US 08/6: 10. APPLICATIO
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	SULT 1 Publication US/101 Publication No. USZO030148972A GENERAL INFORMATION: APPLICANT: Thomas, Wins DEAVING, Denn Feder, John GAITKE, Andr Ruddy, David TRUCHIABRI, WOLIF, ROGET TITLE OF INVENTION: Her NUMBER OF SEQUENCES: 79 CORRESPONDENCE ADDRESS: 79 CORRESPONDENCE ADDRESS: 79 CONTRY: New York COUNTRY: USA ZIP: 10036-2711 COMPUTER: READABLE FORM: MEDIUM TYPE: Flopp COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PAPENTION OF APPLICATION NUMBER FILING DATE: 04-AP APPLICATION NUMBER FILING DATE: 16-AP APPLICATION NUMBER
20 21 21 21 21 21 21 21 21 21 21 21 21 21	1 138-888-9 ence 9, Appl foation No. NEGALIONO. NUMBER OF CORRESPON STRE STRE CIPY COMPUTER CONFORMENT STRE CONFORMENT STRE CIPY CONFORMENT STRE CONFORMENT STRE CONFORMENT STRE CONFORMENT STRE CONFORMENT STRE CONFORMENT STRE CONFORMENT STRE CONFORMENT STRE CONFORMENT FILLI FI
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100.0%; Score 264; DB 13; Length 1440;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;
Matches 264; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                               LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
                                NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 780-9090
TELEPAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDENESS: single
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SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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US-10-138-888-10
; Sequence 10, Application US/1013888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Feder, John N.
; Gairke, Andreas
FILING DATE: 04-APR-1996
                    ATTORNEY/AGENT INFORMATION:
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222..1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
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                                                                                                                                                                                                            COUNTER READABLE FORM:

MUDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPAtible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: THE PC COMPATIBLE

COMPUTER: THE PC COMPATIBLE

COMPUTER: THE PC COMPATIBLE

COMPUTER: THE PC COMPATIBLE

COMPUTER: THE PC COMPATIBLE

COMPUTER: THE PC COMPATIBLE

COMPUTER: THE PC COMPATIBLE

APPLICATION NUMBER: US (08/834,497)

FILING DATE: 04-APR-1996

APPLICATION NUMBER: US (08/632,673)

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US (08/632,673)

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US (08/632,673)

FILING DATE: 16-APR-1996

ATTORNAY AGENT INFORMATION:

ATTORNAY AGENT INFORMATION:
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Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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Pred. No. 1.2e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. +-
0; Mismatches
                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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OTHER INFORMATION: /phenotyp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brian M. Poissant
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SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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TELEFAX: (212) 869-8864
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STRANDEDNESS: single
                                                                                           NUMBER OF SEQUENCES: 79
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Best Local Similarity 100.
Matches 264; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PCC compatible
COMPUTER: IBM PCC compatible
COMPUTER: IBM PCC compatible
COMPUTER: IBM PCC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION: CUNKNOWN>
FILING DATE: 04-MAY-1997
FILING DATE: 04-MAY-1996
FILING DATE: 04-MAY-1996
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/652,265
FILING NUMBER: US 08/652,265
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Ruddy, David
Tsuchinashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                     100.0%; Score 264; DB 14;
100.0%; Pred. No. 2.2e-83;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILLING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
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APPLICANT: Thomas, Winston J.
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                                                                                                                              FEATURE:

NAME/KEY: misc feature

LOCATION: (5885)...(5885)

OTHER INFORMATION: n=a, c, g or US-10-016-634A-25
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CORRESPONDENCE ADDRESS:
                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (5780) ..(5780)
OTHER INFORMATION: n=a, c,
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Matches 264; Conservative
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     ORGANISM: Homo sapiens
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US-10-016-634A-25
Sequence 25, Application US/10016634A
PUBLICATION NO. US20020192666A1
GENERAL INFORMATION:
APPLICANT: Sun, Vongaming
APPLICANT: Recipon, Herve
APPLICANT: Compositions and Methods Relating to Colon Specific Genes and Profile Reference: DEX-0255
TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Profile Reference: DEX-0255
CURRENT APPLICATION NUMBER: US/10/016,634A
CURRENT FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: US 60/244,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 316
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Sequence 1, Application US/09981606

Publication No. US20030129595A1

GENERAL INFORMATION:

TITLE OF INVENTION: Mutations associated with iron disorders

TITLE OF INVENTION: Mutations associated with iron disorders

TITLE OF INVENTION: WHORER: US/09/981,606

CURRENT FILING DATE: 2002-10-16

PRIOR PELIGN NUMBER: 09/277,457

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 30

SOSTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 264; DB 13; Length 2506; Best Local Similarity 100.0%; Pred. No. 1.5e-83; Matches 264; Conservative 0; Mismatches 0; Indels 0;
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                                                                                241 TGGAAATCACAACCACAGCAAGG 264
                                                                                                                                 538 reganantcacancacaecaaee 561
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-981-606-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2506
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LENGTH: 5982
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Sequence 27, Application US/09981606 Publication No. US20030129595A1 GENERAL INFORMATION:
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                 NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 790-9090
TELEPRONE: (212) 790-9064
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                              (HH) protein"
/note= "No. US20030148972Almal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                     /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.

Dayan, Dennis T.
Freder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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ATTORNEY/AGENT INFORMATION:
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US-10-138-888-3
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                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/138, 888
FILING DATE: 02-May-2002
CLASSIFICATION: «Unknown»
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gene 24dl allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brian M. Poissant
REGISTRATION WUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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TELEFAX: (212) 869-8864
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                      STATE: New York
CITY: New York
                                             USA
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Wolff, Roger K.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
HEMOCHROMATOSIS GENE
                                                                                                                                                                                                                                                                                                                                                               ;
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APPLICANT: Rothenberg et al.

TITLE OF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: U5/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 199-03-26
NUMBER OF SEQ. ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2.1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
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APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/852,495C
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100.0%; Pred. No. 3(); ve 0; Mismatchel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-301-844-1/c; Sequence 1, Application US/10301844; Publication No. US20030100747A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 264; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-981-606-27
                                                                                                                                                                                                                     LENGTH: 12146
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43208 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43149
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Publication No. US20030100747A1
GENERAL INFORMATION:
APPLICANT: Ruddy, David A.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
HOLFE, ROGER K.
HEMOCHROMATOSIS GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 235033;
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MEDIUM TYPE: Floppy disk
COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMP
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NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
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STREET: 1155 Avenue of the Americas
CITY: New York
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 235033 base pairs
TELECOMMUNICATION INFORMATION TELEPHONE: 650-493-4935
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                                                                                    TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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US-10-301-844-2/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                            61 IGTITGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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                                                                                                                                                                                                                                    100.0%; Score 264; DB 15; Length 237326; 100.0%; Pred. No. 1.1e-82;
                                                                                                                                                                                                                                                                                Indels
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Publication No. US20030148972A1
GENERAL INFORMATIONS, Winston J.
APPLICANT: Thomas, Winston J.
Feder, John N.
Feder, John N.
Gnirke, Adreas
Ruddy, David
Trachihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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MEDIUM TYPE: Floppy disk
COMFUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKnown>
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                                                                0; Mismatches
                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 237326 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43098 TGGAAAATCACAACCACAGCAAGG 43075
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TELEFAX: 650-493-5556
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Matches 264; Conservative
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US-10-138-888-11
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61 IGITIGAAGCITIGGGCIACGIGGAIGACCAGCIGIICGIGIICIAIGAICAIGAGAGIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-138-888-12
; Sequence 12, Application US/10138888
; Publication No. US2003148972A1
; GENERAL INFORMATION:
Drayna, Winston J.
Preder, John N.
Grirke, Andreas
Ruddy, David
Tsuchhash, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITRET: New York
COUNTRY: USA
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                                                         NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR EDE ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.4%; Score 262.4; DB 1
99.6%; Pred. No. 4.5e-83;
live 0; Mismatches 1
APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-138-888-11
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                      FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 222..1268
                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: replace (4 other information:
                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: allele
NAME/KEY: replac
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.6°
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= 24d2
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1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                   Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Woger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
99.4%; Score 262.4; DB 1.
Best Local Similarity 99.6%; Pred. No. 4.5e-83;
Matches 263; Conservative 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-May-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NATURER: US 08/634,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-May-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= 24d7
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: replace(414, "t")
OTHER INFORMATION: /phenoty
  538 TGGAAATCACAACCACAGCAAGG 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 890
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                  Sequence 77, Application US/10138888 Publication No. US20030148972A1 GENERAL INFORMATION:
                                                                                                                                                                                              APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
222..1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 77: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                US-10-138-888-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%; Score 262.4; DB 13; Length 1440; 99.6%; Pred. No. 4.5e-83;
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                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.5e-83;
0; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brian M. Poissant
REGISTRATION WUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAAATCACAACCACAGGAAGG 264
                                                                                                                                                                                              FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: replace (408, OTHER INFORMATION: /phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-86
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
222. 1268
                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.6
Matches 263; Conservative
ZIP: 10036-2711
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REGISTRATION NUMBER: 28,462
REFERRNCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
 ;
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-138-088-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4002 TGGAAATCACAACCACAGGAAGG 4025
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APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                                                                                           99.4%;
                                                                                           Query Match
Best Local Similarity 99.6
Matches: 263; Conservative
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US-10-138-888-7
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298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAAGAGGAGGACCTTGGTCTTTCCT
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COMPUTER READMELE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888

FILING DATE: 02-May-2002

CLASSIFICATION NUMBER: US/88/834,497

FILING DATE: 04-APR-1997

APPLICATION NUMBER: US 08/652,265

FILING DATE: 23-May-1996

APPLICATION NUMBER: US 08/652,265

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/652,265

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wollff, Roger K.
DY INVENTION: Hereditary Hemochromatosis Gene
OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Hereditary Hemochromatosis (HH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                   241 TGGAAATCACAACCACAGCAAGG 264
                                                                                                                                                                                                                                                                                                                  538 TGGAAAATCACAACCACAGCAAGG 561
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TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thomas, Winston J. Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-10-138-888-5
; GENERAL INFORMATION:
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                                                                                                                                 3762 GITCACACICICIGCACIACTICAIGGGIGCCICAGAGCAGGACCITGGICITICCI
                                                                                                    1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                     Gaps
Length 10825;
                                                     0;
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                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TILE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
  Score 262.4; DB 13;
Pred. No. 1.1e-82;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
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                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: replace(5834, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
TELEFAX: (212) 869-8864
OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing both the 24d1
and 24d2 mutations"
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al Similarity 99.4%; Score 262.4; DB 13; Length 10825;
al Similarity 99.6%; Pred. No. 1.1e-82;
263; Conservative 0; Mismatches 1; Indels 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
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Ruddy, David
Tsudy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                            and 24d2 mutations"
//note="Mereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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Feder, John N.
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APPLICANT: Thom
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NAME/KEY:
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US-10-138-888-79
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                                                                                                                                                                                                                                                                                                                                                                       (HH) protein containing the 24d7 mutation"
/note= "Hereditary Hemochromatosis
/note= "Hereditary Hemochromatosis
(H) gene 24d7 allele"
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                                                                                                                                                                                                                                                           NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRAX: (212) 869-8864
                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
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SEQUENCE DESCRIPTION: SEQ ID NO: 79:
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LOCATION: replace(3878, "t")
OTHER INFORMATION: /phenotype
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02-May-2002
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Best Local Similarity 99.64
Matches 263; Conservative
                       CLASSIFICATION:
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Sequence 10, Appl
Sequence 9, Appli
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-834-4497A-10
US-09-503-444A-10
US-09-679-7457-1
US-08-652-265-1
US-08-652-265-1
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US-08-834-497A-1
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US-08-652-265-7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Perfect score:
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STATE: California
COUNTRY: USA
ZUE: San Francisco
STATE: California
COUNTRY: USA
ZUE: 94111-3834
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION STATE
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMULCATION INFORMATION:
TELEFRAM: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10140 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Dennis T.
APPLICANT: Peder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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San Francisco
                                                           US-09-503-444A-7

US-09-503-444A-7

US-09-216-07-7

US-09-164-023-22

US-08-09-719-5

US-08-09-719-5

US-08-714-025A-4

US-08-244-031-4

US-08-244-031-1

US-08-244-031-1

US-08-31-4

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222..1268
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       TOPOLOGY: li:
MOLECULE TYPE:
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STREET: TWO
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LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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241 TGGAAATCACAACCACAGCAAGG 264
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Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wilf, Roger K.
TITLE OF INTENTION: HEREDITARY INTHESE OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 222..1268
                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                          linear
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STATE: New York
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                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
                                                                                                                                                                                                                        TOPOLOGY:
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| Patent No. 6025130
| GENERAL INFORMATION:
| APPLICANT: Thomas, Winston J. APPLICANT: Prayna, Dennis T. APPLICANT: Peder, John N. APPLICANT: Reder, John N. APPLICANT: Ruddy, David APPLICANT: Teuchihashi, Zenta APPLICANT: Teuchihashi, Zenta APPLICANT: Wolff, Weger K. ITLE OF INVENTION: Hereditary Hemochromatosis Gene
/phenotype= "normal or wild-type (unaffected)"
/label= 24d2
                                                                                                                       /phenotype= "normal or wild-type (unaffected)"
/label= 24d7
                                                                                                                                                                            FEATURE:
NAME/KEY: allele
NAME/KEY: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type of the information: /phenotype= "normal or wild-type of the information: /label= 24d1
US-08-652-265-9
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COUNTY: USA

ZIP: 94111-3834

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265

FILING DATE: 23-MAY-1996

CLASSIFICATION: 514
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100.0%; Pred. No. 2.5e-79;
iive 0; Mismatches 0;
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                                                                                                  LOCATION: replace (414, "a")
OTHER INFORMATION: /phenotyy
OTHER INFORMATION: /unaffect
OTHER INFORMATION: /label= &
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
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OTHER INFORMATION:
OTHER INFORMATION:
                                                             FEATURE:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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US-08-652-265-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 264; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.5e-79;
Matches 264; Conservative 0; Mismatches 0;
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REPRENCED COKET UNMER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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1155 Avenue of the Americas
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478 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537
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APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Ruchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
SUPPRESSE: Pennie E PJ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER TRAINABLE FORMY
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFFATING SYSTEM: Windows 95
SOFFATING SYSTEM: Windows Version 2.0b
SOFFATING NUBBE: US/08/934,497A
FILING DATE: 04-APR-1997
FILING DATE: 04-APR-1997
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: US 08/652,265
FILING DATE: 13-MAY-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATE:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATE:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                      241 TGGAAATCACAACCACAGCAAGG 264
                                                                                                                                                                     538 TGGAAAATCACAACCACAGGAAGG 561
                                                                                                                                                                                                                                                                  RESULT 4
US-08-34-497A-10
. Sequence 10, Application US/08834497A
, Patent No. 6146305
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OTHER INFORMATION: /phenotypo
OTHER INFORMATION:
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TELEX: 66141 PENNIE
INCOMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
FYPE: nucleic acid
STRANDENNES.
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ZIP: 10036-2811
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LOCATION:
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Best Local Similarity 100.0%; Pred. No. 2.5e-79;
Matches 264; Conservative 0; Mismatches 0; Indels 0
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NAME/KEY: allele
LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /phenotype= "normal or wild-type
(unaffected)"
/label= 24d1
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                OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8907-0056-999
                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/034,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: 28,462
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: 28,462
REFERENCE COCKET NUMBER: 28,462
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REFERENCE COCKET NUMBER: 28,462
REFERENCE CASASTION NOWER: SECONDATION: CASASTION NUMBER: SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION OF SECONDATION
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/label= 24d2
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LOCATION: replace(408, "c")
OTHER INFORMATION: (paffec
OTHER INFORMATION: (label=
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222..1268
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NAME/KEY: allele
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LOCATION:
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181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /label= 24d7
FRATURE:
NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /label= 24d1
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OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d2
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NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 264; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.5e-79;
Matches 264; Conservative 0; Mismatches 0;
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Patent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Reder, John N.
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
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                       TELEX: 66141
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 1440 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
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     212-869-9741
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LOCATION: 222..1268
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     TELEFAX:
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                                                                                                                                                                         GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                       Query Match
100.0%; Score 264; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.5e-79;
Matches 264; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Feder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23 *May-1996
FILING DATE: 33 *May-1996
PRIOR APPLICATION NUMBER: 08/632,673
FILING DATE: 16 *Apr-1996
PRIOR APPLICATION NUMBER: 08/630,912
APPLICATION NUMBER: 08/630,912
FILING DATE: 04 *Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSART, BRIAN M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TGGAAAATCACAACCACAGGAAGG 264
; OTHER INFORMATION: /label= 24dl
US-08-834-497A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 9, Application US/09503444A; Patent No. 6228594
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Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Thomas,
APPLICANT: Drayna,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New COUNTRY: US. ZIP: 10036
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US-09-503-444A-9
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61 TGTTTGAAGCTTTGGGCTACGTGAACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTTGACTTCTGGACTATTA 316
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                                                                                                             GENERAL INFORMATION:
APPLICANT: Rothenberg, Barry B.
APPLICANT: Rothenberg, Barry B.
APPLICANT: Sawada-Hiral, Ritsuko
APPLICANT: Barron, James C.
TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
FILE REFERRENCE: 10653/002001
CURRENT APPLICATION NUMBER: U5/09/277,457
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2506;
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APPLICANT: Sawada-Hirai, Ritsuko
APPLICANT: Barton, James C.
TITLE OF INVENTIONS: MUTANTIONS ASSOCIATED WITH IRON DISORDERS
FILE REFERENCE: 24065-004 DIV
CURRENT APPLICATION NUMBER: US/09/679,729
CURRENT FILING DATE: 2000-10-04
PRIOR PLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i LOCATION: (0)...(0)
i OTHER INFORMATION: Missense mutation at nucleotide 314
US-09-277-457-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 264; DB 4; 100.0%; Pred. No. 3.2e-79;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2506
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; Sequence 1, Application US/09679729
; Patent No. 6509442
; GENERAL INFORMATION:
                                                                    Sequence 1, Application US/09277457; Patent No. 6355425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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NAME/KEY: mutation
                                               JS-09-277-457-1
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                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
APPLICATION NUMBER: 08/630,912
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISMATION:
NAME: POISMATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELEFRAN: 212-869-9741
                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
): 1155 Avenue of the Americas
New York
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CTHER INFORMATION: /phenotype=
CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION: /label= 24d1
US-09-503-444A-10
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                        COMPUTER READABLE FORM MEDIUM TYPE: Floppy
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Best Local Simi:
Matches 264;
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/note= "No. 6025130mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
allele"
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NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
COTHER INFORMATION:
OTHER INFORMATION: /note= "No. 6025130mal or wild-type (unaf OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                               genomic
24d2(C)
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24d1(G)
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                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -
LOCATION: 3852..3891
OTHER INFORMATION: / hote= "start and stop positions OTHER INFORMATION: normal or wild-type (unaffected) OTHER INFORMATION: sequence surrounding variant for OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 5507..6023

OTHER INFORMATION: /note= "start and stop positions

OTHER INFORMATION: normal or wild-type (unaffected)

OTHER INFORMATION: sequence surrounding variant for

OTHER INFORMATION: allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                   LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions OTHER INFORMATION: normal or wild-type (unaffected) OTHER INFORMATION: cDNA (SEQ ID NO:9)"
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(unaffected)"
/label= 2442
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(unaffected)"
/label= 24d1
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100.0%; Pred. No. 6.2e-79;
ive 0; Mismatches 0;
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OTHER INFORMATION: /phenotype
OTHER INFORMATION: /unaffecte
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OTHER INPORMATION: (unaffector)
OTHER INFORMATION: (lanffector)
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OTHER INFORMATION: (unaffecte
OTHER INFORMATION: (lnaffecte
OTHER INFORMATION: /label= 24
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Best Local Similarity 100.
Matches 264; Conservative
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LOCATION:
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NAME/KEY:
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                                                                                                                                                                                                                  77 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 136
                                                                                                                                                                                                                                                                                                             137 TGTTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 196
                                                                                                                                                                                                                                                                                                                                                                                                        197 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCCAGATGTGGCTGC
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                                                                                                                                                                     GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTC
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                                                                       Length 2506;
                                                                                                                      Indels
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) Patent No. 6025130
) GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Peder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Trechihashi, Zenta
APPLICANT: Houchihashi, Zenta
APPLICANT: Wolff, Roger K.
ITILE OF INVENTION: Hereditary Hemochromatosis Gene
       ; OTHER INFORMATION: Missense mutation at nucleotide 314
US-09-679-729-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                       Query Match
100.0%; Score 264; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.2e-79;
Matches 264; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17957-000500
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid STRANDEDNESS: single
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CORRESPONDENCE ADDRESS
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US-08-652-265-1
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/phenotype= "Hereditary Hemochromatosis
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
APPLICATION NUMBER: US 08/652,265
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
PLIASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                 /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08834497A Patent No. 6140305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Winston J. APPLICANT: Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               Matches 264; Conservative
; OTHER INFORMATION:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-652-265-3
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-834-497A-1
                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)
COTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: mutation"
OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)
OTHER INFORMATION: gene 24d1 allele"
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LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: -
LOCATION: 140..7319

OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INPORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
                                                                                                                      APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Peder, John N.
APPLICANT: Peder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Hordinash!, Zenta
APPLICANT: Hordinash: Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCES: 44
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Two Enbarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUDNITAY: U.S.3.4

CUNTRAY: U.S.3.4

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: BACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: S14

ATTORNEY/AGENT INFORMATION: REGISTRATION: NUMBER: 30,23

REFERENCE/DOCKET NUMBER: 17957-000500

TELEROMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: STG-0300

INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 10825 base pairs TYPE: mochaic acid stringle stringle.
                                                 Sequence 3, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: replace(5834, "a")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3852..3891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                               US-08-652-265-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
                                                                                                                                                                                                                                                                                                                        3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGAGAGTC 3881
                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                           61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
                                                                                                                                                                       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                           121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
                                                                                                                               1 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                   Gaps
                                                                   .
0
100.0%; Score 264; DB 3; Length 10825; 100.0%; Pred. No. 6.2e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Feder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tauchihashi, Zenta
APPLICANT: Tauchihashi, Zenta
APPLICANT: Tauchihashi, Zenta
APPLICANT: HERBITANY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCES 76
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-ARR-1997
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3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881
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ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-834-497A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: N
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "No. 6140305mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
allele"
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COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d1(G) OTHER INFORMATION: allele (SEQ ID NO:20)"
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: footo.6153, 7107..7147)
LOCATION: footo.6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis oTHER INFORMATION: /note= "No. 6140305mal or wild-type (unafOTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: 3-
LOCATION: 3952..3891
LOCATION: 3952..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) OTHER INFORMATION: allele (SEQ ID NO:41)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: -
LOCATION: 140..7319
COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: cDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: replace(3872, "c")

LOCATION: replace(3872, "c")

OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /label= 24d2

FEATURE:

NAME/KEY: allele
LOCATION: replace(3878, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /label= 24d7

FEATURE:
NAME/KEY: allele
LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /label= 24d1
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Best Local Similarity 100.0%; Pred. No. 6.2e-79;
Matches 264; Conservative 0; Mismatches 0;
                                                               8907-0056-999
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMULICATION INFORMATION:
TELEPHONE: 650-493-4935
TELERA: 650-493-5556
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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3882 GCCGTGTGGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGGCTGC 3941
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121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
                                                                                                                                                                                       181 AGCTGAGTCTGAAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Dennis T.
APPLICANT: Peder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Worlf, Roger K.
TILLE OF INVENTOR: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FRAFESO for Windows 95
SOFTWARE: PARESO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION STAR
APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY AGENT THORMATION:
WANDED THE DATE: DATE OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Pennie & Edmonds LLP
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4002 resaharcachaccachechase 4025
                                                                                                                                                                                                                                                                                                                                                                                        241 TGGAAATCACAACCACAGCAAGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08834497A Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: POISSAIL, BRIAN M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 890
'TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELERAX: 650-493-555-6
TELERAX: 6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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USA
                                                                                                                                                                             10036
                                                                                      STATE: Ne COUNTRY: ZIP: 100:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3762 GTTCACACTCTCTGCACTCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | NAME/KEY: allele | LOCATION: replace(5834, "a") | OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /phenotype= "Grand Trock of The Trock of The Trock of The Trock of The Trock of The Trock of The Trock of The Trock of The Trock of The Trock of The Trock of The Trock of The Trock of The Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of Trock of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 3852..3891
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "start and stop positions for
genomic sequence surrounding variant
for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Hereditary Hemochromatosis Gene NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4002 TGGAAATCACAACCACAGCAAGG 4025
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Patent No. 6228594
GENERALI INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
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Best Local Similarity 100.8
Matches 264; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             140..7319
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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(unaffected)
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "No. 6228594mal or wild-type (unafOTHER INFORMATION: /note= "No. 6228594mal or wild-type (unafOTHER INFORMATION: allele"
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LOCATION: 3852..3891
OTHER INFORMATION: // note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) OTHER INFORMATION: allele (SEQ ID NO:41)"
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OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION:
TELEPHONE: 212-790-909
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                OPERATING SISTEM: WITHOWS 95
SOFTWARE: WordPerfect Version B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28,462
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Poissant, Brian M
REGISTRATION NUMBER: 28
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LOCATION: 5507..6023
OTHER INFORMATION: /r
OTHER INFORMATION: nc
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                        100.0%; Score 264; DB 3; Length 10825; 100.0%; Pred. No. 6.2e-79; cive 0; Mismatches 0; Indels 0;
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US-09-503-444A-3
i Sequence 3, Application US/09503444A
j Patent No. 6228594
j GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
ITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                NAME/KEY: allele
LOCATION: replace(5834, "g")
OTHER INFORMATION: 'Dhenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                                                                 /phenotype= "normal or wild-type
(unaffected)"
/label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4002 regalantcachaccachechaec 4025
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TGGAAAATCACAACCACAGCAAGG 264
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APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
/label= 24d2
                                                          LOCATION: replace (3878, "a")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffect
OTHER INFORMATION: /label= 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100. Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
                                        NAME/KEY: allele
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                                                                                                                                                                                                                                                                             US-09-503-444A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GITCACACICICIGCACIACCICITCAIGGIGCCICAGAGCAGGACCIIGGICITICCI
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis
OTHER INFORMATION: mutation"
OTHER INFORMATION: /note= "Hereditary H~-
OTHER INFORMATION: gene 24d1 all
EBATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e-79;
Matches 264; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: replace(5834, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: -
LOCATION: 3852..3891

LOCATION: /note= "start and stop positions for OTHER INFORMATION: qenomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: -
LOCATION: 5507..6023
CTHEN INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
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TELEX: 66141
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 10825 base pairs TYPE: nucleic acid
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3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
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US-09-277-457-27

$ Sequence 27, Application US/09277457

$ Patent No. 6355425

$ GENERAL INFORMATION:

$ APPLICANT: Rothenberg, Barry E.

$ APPLICANT: Barcon, James C.

$ TILLE OF INVENTION: WITATIONS ASSOCIATED WITH IRON DISORDERS

$ TILLE OF INVENTION: WUTATIONS ASSOCIATED WITH IRON DISORDERS

$ TILLE OF INVENTION: WUTATIONS ASSOCIATED WITH IRON DISORDERS

$ TILLE OF INVENTION: WUTATIONS ASSOCIATED WITH IRON DISORDERS

$ TILLE OF INVENTION: WUTABER: US/09/277,457

CURRENT FILING DATE: 1999-03-26

$ SOFTWARE: FASLSEQ for Windows Version 4.0

$ SEQ ID NO 27

**ILENGTH 12146
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100.0%; Score 264; DB 4; Length 12146;
Best Local Similarity 100.0%; Pred. No. 6.5e-79;
Matches 264; Conservative 0; Mismatches 0; Indels 0;
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                                                                                               4002 TGGAAAATCACAACCACAGCAAGG 4025
                                                       241 TGGAAAATCACAACCACAGGAAGG 264
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CRGANISM: Homo Sapiens
US-09-277-457-27
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4652 GITCACACICICIGCACIACCICITICALIGATICA GAGAGCAGGACCITIGATICA 4711

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4712 IGTTIGAAGCTTIGGGCTACGIGGAIGACCAGCTGTTCGIGTTCTAIGATCAIGAGAGIC 4771

61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGAGAGTC-120

4772 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 4831

121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180

Search completed: February 11, 2004, 17:12:24 Job time : 34.2837 secs

TGGAAAATCACAACCACAGCAAGG 4915

241 TGGAAATCACAACCACAGCAAGG 264

181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240

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score greater than or equal to the score of the result being printed,
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434
1 tgcctcctttggtgaaggtg.....acttgcttttctgtttag 434
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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	oo c	276	63.6	860	σ 0	AY205604	AY205604 Homo s
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	LOCUS.			4	- 1	12146 bp DNA	linear PAT 20-APR-2002
(i∕~	CESSION		AR199263	mori /	parent	VUS 635542	
	VERSION	AR1	99263.1	GI:2024	2493	131	
	SOURCE		Unknown.		/		
į	ORGANISM		Unclassified.	ed.	ĺ		
킾	AUTHORS	Roth	(bases penberg	B.E.	L4to, Spike	1 (bases 1 to 12146) Rothenberg, B.E., Sawada-Hirai,R. and Barto	Barton, J. C.
	TITLE	Muta	tions	associa	ted	with iron disorders	
ċ	JOURNAL	Pate	ent: US	635542	5-A	27 12-MAR-2002;	

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Bases 1 to 888) Albig, W., Drabent, B., Burmester, N., Bode, C. and Doenecke, D. The haemochromatosis candidate gene HFE (HLA-H) of man and mouse is located in syntenic regions within the histone gene cluster 98208340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-1999
                                                                                                                                                                                                                                                                                                   241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Submitted (14-MAR-1997) Albig W., Georg-August-Universitaet
Goettingen, Biochemie und Molekulare Zellbiologie, Humboldtallee
23, Goettingen, FRG, 37073
Locating.
                                    6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGG
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            121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGG
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'note="haemochromatosis candidate
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/clone lib="ICRF YAC-library"
1028. .10637
gene="HFE"
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db_xref="GI:1890180"
db_xref="SWISS-PROT:Q30201"
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| Organism="Homo sapiens"
| Mol_type="genomic DNA"
| db_xref="taxon:9606"
| /chromosome="6"
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6928. .7041;7995. .8035)
/gene="HFE"
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haemochromatosis; HFE gene.
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Rothenberg, B.E., Sawada-Hirai, R. and Bart
Mutations associated with iron disorders
Patent: US 6509442-A 27 21-JAN-2003;
Location/Qualifiers
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6554 GGGCCTTGAACTACTCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 6613
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Direct Submission
Submitted (04-DEC-1996) P. Gasparini, Servizio de Genetica Medica
IRCCS, 'Ospedale CSS', Via Cappuccini, 71013 S Giovanni, Rotondo
(FG), ITALY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG
                                                      6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG
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Y09803.1 GI:2370113
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2 (bases 1 to 653)
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### Accaged Similarity ### Seed No. 1.8e-129; ####################################	QY 301 GCTGAGAAATCTATTGGGGGTTGAGAGGGAGTGCCTGAGGAGTTATTTGGGAGTGAGA 360 Db 351 GCTGAGAAATCTTTTGGGGGTTGAGAGAGTGCTGAGAGTAATTATGGCAGTGAGA 410 QY 361 TGAGGAATCTGCTCTTTGTTAGGGGTTGGGAGGGGAATCAAAGGCTTTAACTTGC 420 Db 411 TGAGGATCTGCTCTTTGTTAGGGGTTGGGCTGGGCAATCAAAGGCTTTAACTTGC 470 Db 421 TTTTTCTGTTTTAG 434 Db 471 TTTTTCTGTTTTAG 484 RESULT 8 A31 TTTTCTGTTTTAG 484	AR117789 10825 bp 100. Sequence 1 from patent US 6140305. ON AR117789 1 GI:14098695 1 AR117789.1 GI:14098695	### COUNT 2998 a 2253 c 2648 g 2926 t Ouery Match Query Match Query Match 99.6%; Score 432.4; DB 6; Length 10825; Best Local Similarity 99.8%; Pred. 0. 0. 2.5e-129; Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Oy 1 TGCCTCCTTTGGTGAAGGTGACACATGTGACCTCTTCAGTGACCACTCTAGGTGTC 0.

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Gaps

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AL359892 193752 bp DNA linear HTG 13-JUN-2001
Homo sapiens chromosome 6 clone RP11-557F22, *** SEQUENCING IN
PROGRESS ***, 18 unordered pieces.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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On Aug 27, 2000 this sequence version replaced gi:9864230.
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                               Thomas's I to 10825)
Thomas'W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228584-A 5 08-MAY-2001;
Location/Qualifiers
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AL1359892.5 GI:9930971
AL359892.5 GI:9930971
HTGS_PHASE1; HTGS_CANCELLED.
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 1 08-MAY-2001;
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                                                                                                 Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 183925 bases at least Q40
Consensus quality: 187703 bases at least Q30
Consensus quality: 189658 bases at least Q30
Insert size: 193053; www-of-contigs
Insert size: 193047; agarose-fp
Quality coverage: 3.68% in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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16 184996: contig of 20661 bp in length

7 185096: gap of 100 bp

17 193752: contig of 8656 bp in length.

Location/Qualifiers
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gap of 100 bp
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/note="assembly_fragment:01752
fragment_chain:1"
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/note="assembly_fragment:01177
fragment_chain:1"
                         Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: bA557F22
  site: http://www.sanger.ac.uk
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/db_xref="taxon:9606"
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/clone="RP11-557F22"
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99.6%; Score 432.4; DB 2;
Best Local Similarity 99.8%; Pred. No. 3.3e-129;
Matches 433; Conservative 0; Mismatches 1;
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|hote="assembly_fragment:00783.0"
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57457. 59445
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158760. .164235
note="assembly_fragment:01675"
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7538. .57356
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PAT 29-SEP-1999

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198209 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 198268
                                               Unclassified.

1 (bases 1 to 246240)

1 (bases 1 to 246240)

Peder, J.Nathan., Kronmal, G.Scott., Lauer, P.M., Ruddy, D.A.,
Thomas, W., Tsuchihashi, Z. and Wolff, R.K.

Megabase transcript map: novel sequences and antibodies thereto
Patent: US 587227-A 20 16-FEB-1999;

1. .246240
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Pred. No. 3.4e-129;
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Sequence 20 from patent
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Feder, V.N., Kronmal, G.S., Lauer, P.M., Ruddy, D.A., Thomas, W.J., Tsuchihashi, Z. and Wolff, R.K.
Polymorphisms and new genes in the region of the human
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/organism="Homo sapiens"
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1 (bases 1 to 246240)
Feder,J.Nathan., Krommal,G.Scott., Lauer,P.M., Ruddy,D.A.,
Fhomas,W., Tsuchihashi,Z. and Wolff,R.K.
Megabbase transcript map: novel sequences and antibodies thereto
Patent: US 5872237-A 21 16-FEB-1999;
Location/Qualifiers
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Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
Thomas,W., Tsuchihashi,Z. and Wolff,R.K.
Megabase transcript map: novel sequences and antibodies th
Patent: US 587227-A 22 16-FEB-1999;
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Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quintana,L., Domingo,R. Jr., Meyer,N.C., Irrinki,A., McClelland,E.E., Fullan,A., Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C., Tsuchihashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J.N. Genome Res. 7 (5), 441-456 (1997)
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Length 246240;
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     DB 6;
Score 432.4; DB 6;
Pred. No. 3.4e-129;
                                                                                                                0; Mismatches
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us-09-981-606-27_copy_6494_6927.rge

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Heterozygote T->C mutation was detected at the intron 4 of the human hemachromatosis gene in an Africa American individual Unpublished (1992) (Leases 1 to 733)

Kutlar, F., Glendenning, M. and Kutlar, A.

Direct Submitssion

Submitted (18-JUN-2002) Medicine/Hematology-Oncology/Hemoglobin DNA Laboratory, Medical College of Georgia, 15th street, AC-1000, Augusta, GA 30912, USA
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product="hereditary hemochromatosis protein precursor"
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Pred. No. 6.1e-129;
0; Mismatches 2;
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gene="HFE"
note="HLA-H protein precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Homo sapiens"
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'replace="t"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   map="6p21.3"
sex="female"
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Best Local Similarity 99.5%;
Matches 432; Conservative
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/gene="HFE"
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AUTHORS
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Homo sapiens hereditary hemochromatosis protein precursor (HFE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGGCCTTGAACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Kutlar, F., Glendenning, M. and Kutlar, A.
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0; Mismatches 1;
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Search completed: February 11, 2004, 16:24:00 Job time: 2121.64 secs

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February 11, 2004, 14:16:30; Search time 1742.84 Seconds (without alignments) 6052.274 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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CB529554 BG747345 BE272926 BM723847

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729 819 570 668

63.6 57.9 56.0 52.1

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AZ025590 RPCI-23-3 AK089986 Mus muscu AK089986 Mus muscu AZ074871 RPCI-23-4 AZ025794 RPCI-23-3 BI452688 G03169877 CB46137 Sn03 F06 CD245288 AGENCOURT BB487497 176270 BA AB005947 Mususe gen BM694948 UT-E-CII- AW514210 hd75505.x BF854420 MIZ-EN009 BF804666 III-C-CII- BH7523297 QV3-CT1055	AW516790 XQ04c07.X AU015930 DKF2D564A A1978886 WF2BC07.X BG425317 60244723 CD355590 UT-H-FT2- A1954031 WX789G95.X BG742120 6026335.X BG742120 6026335.X BG742120 60262342 BW985243 UT-CF-EC1 CB528356 UT-H-FT2- BG681220 602623749 CD24539 AGENCOURT BG744821 602722944 B1185105 UNL-P-FN-BG682596 60262374 CD517051 AGENCOURT AL561819 AL561819 A1557260 PT2.1 15 BG68254 AGENCOURT BG744157 602722954 AL564088 AL540488 AL580556 AL580556 AL57498 AL540488 AL580556 AL580556 AL57498 AL540488 AL580556 AL580556 AL574988 AL540488 AL580556 AL580556 AL574938 BF038899 CO1461404 BG165057 602722954	mRNA linear EST AP FT2 Homo sapiens cDN sequence. aniata; Vertebrata; Eut arrhin; Hominidae; Ho gov/ncicgap. r Genome Anatomy Projec fonome Anatomy Projec sonome, University of I Bento Soares, University of soares, University of n information can be fo
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/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="MIH MGC_15"
/lone lib="MIH MGC_15"
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(Stratagene) and Supersoript II RT (Life Technologies)"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM240 row: j column: 04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          573 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCA-G
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National Institutes of Health, Mammalian Gene Collection (MGC)
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0; Mismatches 1; Indels 2;
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                      /organism="Homo sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4857941"
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                                                                                                                                                                                                                                                                                                                            /clone_lib="NCIC CGAP FT2"
| /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site.1: EcoR 1; Site.2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from a pool 6 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
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1 (bases 1 to 819)
NHI-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Best Local Similarity 100.0%; Pred. No. 5.7e-67;
Matches 276; Conservative 0; Mismatches 0; Indels
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TAG_TISSUB=Human Lung Aveolar Macrophage
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/lab_host="DH10B (Life Technologies)"
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                                                                                organism="Homo sapiens"
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
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UI-E-EO1-aix-h-17-0-UI.rl UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-aix-h-17-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Iowa 375 Newton Road , 4156 MEBRE, Iowa City, IA 52242, USA Tel: 319 335 8565 Fax: 319 335 9565 Email: bento-soares@miowa.edu
                                                                                                                                                                                                                                                                                                                           56.0%; Score 243; DB 10; Length 570; 100.0%; Pred. No. 1.1e-57; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coordinated Laboratory for Computational Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
                                            organism="Homo sapiens"
High quality sequence stop: 566.
Location/Qualifiers
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/note="Organ: eps. Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UT-E-EO1 is a normalized CDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oilgo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGGGGTARAC: This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NBI)."
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CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa Dna Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: M. Bento Soares, University of Iowa Clone Distribution: Magearchers may obtain clones from Research Seq primer: M.3 Reverse.
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1 (bases 1 to 444)
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Pred. No. 7.1e-53;
                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EO1-aix-h-17-0-UI"
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100.0%; Pred. No. /.-.
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                                                                                                                                                                                                                                   1. .668
/organism="Homo sapiens"
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/lab_host="DH10B (Life
/clone_lib="UI-E-E01"
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            Contect: Shaying Zhao
Contect: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 3010 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Bex="Female"
/lab_host="DH10B"
/clone lib="RPCI-23"
/note="Corgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Corgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
BCoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-23-316A10"
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VDFWTIMGNYNHSKYTKLGYVSESHILQVVLGCEVHEDNSTSGFWRYGYDGQDHLEFC
PKTLINWSARDEGAWATKVEWDEHKIRAKQNRDYLEKOCPEQLKRLLELGRGYLGQQVP
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GWLTLLAVAPGDBTRFFCQVZEHPGLPQPLTASWEPLQSQAMIIGIISGVTVCAIFLVGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="thymic cells"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev_stage="2 days neonate"
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                          CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Center for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.
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/db xref="G1:26354116"
/translation="MSLSAGLPVRPLLLLLLLMSVAPQALPPRSHSLRYLFMGASEPD
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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RPCI-23-408J22.TJ RPCI-23 Mus musculus genomic clone RPCI-23-408J22 AZ074871
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/lab host="DHIOB"
/clone lib="RPG1-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
BroRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
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Mouse BAC End Sequences from Library RPCI-23
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/crderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
pittp://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Addical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/organism="Mus musculus"
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/clone="RPCI-23-408J22"
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/strain="C57BL/6J"
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          Matches 207; Conservative
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Class: BAC ends.
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QGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWBPLQSQAMIIGIISGVTVCAIFLVG
ILFLILRKRKASGGTMGGYVLTDCE"
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Dlglplfeargyvddolfvsynhesrraeprapwilegtssolwlhlsoslkgwdymf
                                                                               Grases 1 to 1723)

Adachi, J. Aizawa, K. Akhhira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, P. Hayatsu, N., Hirancho, K., Hiraoka, T., Hori, F. Inchani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukwa, T., Kato, H., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matunyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Shibata, Y., Shinagawa, A., Shizaki, T., Sogabe, Y., Shibata, Y., Tagami, M., Tagami, M., Tagama, A., Shizaki, T., Tanaka, T., Tejima, Y., Toya, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Subnistion Research Group, RIKEN Genome Caiter (GSC), RIKEN Yokohama Institute; 1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Richtp://genome-res@gsc.riken.go.jp, URL: http://genome-res@gsc.riken.go.jp, Please visit our web site (http://genome-res@gsc.riken.go.jp, Please visit our web site (http://genome-gsc.riken.go.jp, Please visit our web site (http://genome-gsc.riken.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'tissue type="tongue"
'clone lib="RIKEN full-length enriched mouse cDNA library"
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db_xref="MGI:1905246"
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/protein_id="BAB26373.1"
/db_xref="GI:12844463"
/db_xref="MGI:109191"
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clone="2310032M04"
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99. .1178
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/strain="C57BL/6J"
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          Nature 420, 563-573 (2002)
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EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " 149 c 124 g 114 t l others
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Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
blate: 316 row: C column: 10
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                    282
                                                                                                                                                                                                                                                                              61 GGGCCTTGAACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
                                                                                                                                                                                                                                                                                                                       281 AGGCTCTGGACTTCTTCCCCCAGAACATCACTATGAGGTGGTTGAAGGACAACCAC 222
                                                                                                                                                                                                                                                                                                                                                                 121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 481)
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                                                                                                                                                                                            1 TGCCTCCTTTGGTGAAGGTGACACATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                                                                                                                                                                                                                         181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
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                                                                                                      35.5%; Score 154; DB 28; Length 536; 74.5%; Pred. No. 1.4e-32; ive 0; Mismatches 70; Indels
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Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 ACCCAGGCCTGGACCAGCCTCTCACTGCGCT 65
                                                                                                                                               0; Mismatches
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/clone="RPCI-23-316C10"
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/strain="C57BL/6J"
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                                                                                                                               Best Local Similarity 74.5
Matches 207; Conservative
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                                                                                                           Query Match
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AZ025784/C
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                                          BASE COUNT
ORIGIN
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
SOURCE
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/Globe="RPCC-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
BCORI, Site 2: BCORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
135 c 112 g 108 t
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603169877F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5249395 5',
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WHI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11629 row: j column: 20
High quality sequence stop: 818.
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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/clone="lthAdB:154935"
/tissue type="tumor, gross tissue"
/dev_stage="7 months"
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/mol_type="mRNA"
/strain="C57BL/63"
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Mus musculus
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al Similarity 73.4%;
204; Conservative
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Gaps

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EST 22-MAY-2003
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National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.B. Consortium/LINL at:

http://image.llnl.gov

Plate: NDAM439 row, p column: 23

High quality sequence stop: 693.
                                                                                                                                                                                                                                                   47 CACTCTACGGTGTCGGGCCTTGAACTACCCCCCAGAACATCACCATGAAGTGGCTGAA
                                                                                                                                                                                                                                                                                                                    609 CACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTAAGGAGATCTCCCTGACCTGGCGGCG
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AGENCOURT 14098873 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30376798 5′, mRNA sequence.
                                                                                                                            Length 611;
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6.1e-14;
ches 95; Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                            DB 14;
                                                                                                                                                          Pred. No. 6.1e
0; Mismatches
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                                                                                                                            88;
No. 6
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/db_xref="taxon:9606"
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sal Similarity 61.7%;
158; Conservative
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Best Local
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JOURNAL
COMMENT
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hote="Vector: pSPORTI; Site 1: NotI; Site 2: SalI;
hote="Vector: pSPORTI; Site 1: NotI; Site 2: SalI;
Library made from pools of polyA selected RNA, isolated at
different times post-infection (0 to 16 hrs) from African
swine fever virus (isolate Pretorisuskop/96/4) infected
swine macrophages. Macrophages were derived from
peripheral blood mononuclear cells cultured for 48 hrs on
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                                                              Sall;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TAACGGGGATGAGACCTATCAAGGCTGGCTGACATTGGCCGTGGCCCCTGGGGACGAGGC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 AAGGTTCACTGTCAAGTGGAGCACCCAGGCCTGGACCAGCCTCTCACTGCCTCTTGGGA 181
                      /clone lib="NCI_CGAP_MamE"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
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PO Box 848, Greenport, NY 11944-848, USA
PO ED 848, Greenport, NY 11944-848, USA
PO ED 848, Greenport, NY 11944-848, USA
Fax: 631 323 3044

Email: jneilan@piadc.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim alt option. Vector identified by cross match v0.999329 and lucy vI.17p.
Seq primer: MI3 Forward.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 611)
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                                                                                                                                                                                                                                                                                                                 Score 105.2; DB 12; Length 831; Pred. No. 9.6e-19; 0; Mismatches 83; Indels 0;
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sn03_F06.f sn Sus scrofa cDNA 5', mRNA sequence.
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Plum Island Animal Disease Center
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/cell_type="macrophage"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9823"
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   lab_host="DH10B"
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   Pred. No. 1.4e-13;
0; Mismatches 99; Indels
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Best Local Similarity 63.4%;
Matches 149; Conservative
   62.1%;
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                       172; Conservative
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/lab_host="DH10B"
/clone_lib="BARC_5BOV"
/note="Vector: pCMV SORT6; Site_1: Not1; Site_2: Sal1;
Library made_from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: tads@lpsi.barc.usda.gov
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                  42 GTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGG 101
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                                                               3;
                           Length 877;
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USDA, ARS, Beltsville Agricultural Research Center
Bd19. 200 Rm 2A, Beltsville, MD 20705, USA
TP1: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE487497 490 bp mRNA linear 176270 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
                                                               85; Indels
                       Score 88; DB 14;
Pred. No. 7e-14;
0; Mismatches 85;
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/mol_type="mRNA"
/db_xref="taxon:9913"
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Plate: 138 row: G column: 4
Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
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                         Query Match 20.3%;
Best Local Similarity 63.3%;
Matches 152; Conservative
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22135956
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ABUUS947 752 bp DNA linear GSS 04-AUG-1997 Mouse genomic DNA, chromosome 17, clone cosmid 12.1, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-JUL-1997) Masayasu Yoshino, U.T. Southwestern Medical
Center, HHM1, 523 Harry Hines Blvd, Dallas, TX 75235-9050, USA
(E-mail:YOSHINO@UTSW.SWHED.EDU, Tel:214-648-5047, Fax:214-648-5453)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 GGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 GCATGCCCAGCACCTCA---CCCAGGACATGCAGCTTGTAGAGACCAGGCCTGCAGGGGA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 CACCCTGAGGTGCTGGGCCCTGGGCTTCTATCCTGCTGACCTCACCCTGACCTGGCAGAA
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196 c 198 g 192 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yoshino, M., Jones, E. and Pischer Lindahl, K. BAC clones from the H2-T region of the 129 mouse, Tlaf Unpublished
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Pred. No. 2.1e-13;
0; Mismatches 83; Indels 3
443
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/mol_type="genomic DNA"
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Mammalia; Eutheria; Rodentia;
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20.0%; Score 86.6; DB 10; Length 490;

Query Match

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/mol_type="mRNA"
/mol_type="mRNA"
/dov_stef="texacn:9606"
/clone="Ul-E-CII-dr-j-06-0-UI"
/tissue_type="RpE and Choroid"
/dav stage="adult"
/dav stage="adult"
/dav stage="bH108 [Life Technologies) (Tl phage resistant)"
/clone_lib="Ul-E-CII"
/lote="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
UI-E-CII is a normalized CDNA library confaining the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) B tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
                                                                                                                                                                                                                                 EST 28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
COOM Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
303 TGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTCTTGGGAAAGAGCAGAGTTACAC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 467)

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                                                                                               363 Argecardreracargaedecreceraadeceercaacereagargaeara
                                                                                                                                                                                                                           BM694948 1inear EST 28
UI-E-CII-afr-j-06-0-UI.rl UI-E-CI1 Homo sapiens CDNA clone
                                                227 GTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coordinated Laboratory for Computational Genomics University of Iowa University of Iowa 775 Newton Road, 4156 MEBRF, Iowa City, IA 52242, 731: 319 335 9565 Fax: 319 335 9665 Email: bento-soares@wiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 t
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19.6%; Score 85.2; DB 12; Length 467; 60.9%; Pred. No. 3.4e-13; Live 0; Mismatches 98; Indels 3;

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149
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92
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Genomic DNA of a h	Human musculoskele	cDNA encoding nove	Hereditary haemoch	Human hereditary h	Human hereditary h	Hereditary haemoch	Human hereditary h
SUMMARIES	a	AAA96794		ABX59735	AAT96690	AAC68425	AAC68427		
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                          6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGG
                                                                                               GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG
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11-JUL-2000;
14-JUL-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the human histocompatibility iron loading (HFE) gene. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of am utation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number U60319). The presence of the mutation indicates the disorder or the genetic susceptibility to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is used to diagnose an iron disorder
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/number= 6
10206..10637
/*tag= m
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                                               /number= 3
6494..6769
/*tag= 9
/number= 3
5401..6493
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/number= 6
                                                                                                                                                                               6928..7041
/*tag= i
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/*tag= j
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2000US-0226279.
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2000US-0226868.
2000US-0227182.
2000US-0227182.
2000US-0228924.
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200005-0239337.
200005-0240960.
200005-024121.
200005-0241785.
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2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-024617.
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2000US-0229344.
2000US-0229345.
2000US-0229509.
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2000US-0230437.
2000US-0230438.
2000US-0231242.
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2000US-0231244.
2000US-0231413.
2000US-0231414.
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2000US-0232397.
2000US-0232398.
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2000US-0237038.
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2000US-0225758.
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2000US-0232081
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2000US-0234998.
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2000US-0236367
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2000US-0236370.
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20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
01-NOV-2000;
                                                                           23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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-SEP-2000;
-SEP-2000;
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08-SEP-2000
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08-SEP-2000
12-SEP-2000
14-SEP-2000
14-SEP-2000
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02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
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Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash SC, Ruben SM
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246521.
08-NOV-2000; 2000US-0246521.
08-NOV-2000; 2000US-02466521.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0249201.
17-NOV-2000; 2000US-0249201.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-024921.
17-NOV-2000; 2000US-024921.
17-NOV-2000; 2000US-024921.
17-NOV-2000; 2000US-024921.
17-NOV-2000; 2000US-024921.
17-NOV-2000; 2000US-024921.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-0251868.
0S-DEC-2000; 2000US-0251868.
0S-DEC-2000; 2000US-0251869.
0S-DEC-2000; 2000US-0251869.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis
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Example 2; SEQ ID NO 3112; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and cher cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases such as wiral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.Wipo.int/pub/published_pot_sequences.

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17-JAN-2001; 2001US-0764877
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re-vascularisation; thrombosis; arteriosclerosis; mineral content;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;
we cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
post-operative tissue repair; limb regeneration; neuronal growth;
well-related complex; chondrocyte growth; bone regeneration;
periodontal regeneration; tissue transport; bone graft; skin aging;
weratinocyte growth; hair loss; melanocyte growth; cell proliferation;
weight; hair colour; eye colour; skin; percentage of adipose tissue;
pigmentation; commetic surgery; metabolism; biorhythm; caricadic rhythm;
depression; tendency for violence; pain; reproductive capability;
whormone level; endocrine level; appetite; libido; memory; stress;
storage capabilty; fat content; lipid content; protein content;
warbohydrate content; vitamin content; cofactor content;
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                                                                                                                                                                             TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 1664
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                                                                                                                                           1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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                                                            Length 5749;
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                 Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;
                                                                                                    Indels
                                                         Score 432.4; DB 22;
Pred. No. 2.8e-121;
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                                                                                                  0; Mismatches
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                                                         99.6%;
99.8%;
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                                                                               Local Similarity
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                                                            Query Match
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US2002147140-A1

10-OCT-2002

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The invention describes an isolated nucleic acid molecule comprising a agequence encoding musulloskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metatrases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriossclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3112; 321pp;
                                                                                        2000US-218290P.
2000US-220963P.
2000US-224518P.
2000US-224518P.
2000US-22567P.
2000US-225267P.
2000US-225268P.
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2000US-225757P.
2000US-226868P.
2000US-228688P.
2000US-22924P.
2000US-229347P.
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2000US-237037P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-128199/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ROSE/) ROSEN C A. (RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                            08-SEP-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                              29-SEP-2000;
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                                                                       11-JUL-2000;
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                                                                                                                                                                                                         22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BARA/)
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Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.

Homo sapiens

Hereditary haemochromatosis gene.

14-APR-1998 (first entry)

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conditions, such as, Alzheimer's dieease, barkinson's dieease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sumburn by transports or bone grafts; prevents skin aging due to sumburn by stimulating keratinocyte growth; prevents hair loss, since FGF family stimulates activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains crgans before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryons; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape colour, skin, percentage of adipose tissue, pigmentation, size, and shape mammal's metal state or physical state by influencing biorhythms, caricadic rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This sequence encodes a novel human content.
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regeneration; stimulates neuronal growth; can treat and prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1725 regareccaaegaerrecaaecraaaeaecrarrececaareseareseaecraecae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculoskeletal system antigen.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGCCTCCTTTGGTGAAGGTGACACATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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                  neuronal damage occurring in certain disorders or neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.6%; Score 432.4; DB 25; Length 5749; 99.8%; Pred. No. 2.8e-121; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tp.seqdata.uspto.gov/sequence.html?DocID=20020147140.
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Matches 433;
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AAT96690 standard; DNA; 10825 BP.

RESULT 4
AAT96690
ID AAT9

AAT96690;

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Hereditary haemochromatosis gene and variants - useful for diagnosis and treatment of hereditary haemochromatosis disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutated form is associated with hereditary haemochromatosis (HH). To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HLA region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of chromosome 6. A physical clone coverage was then generated extending from D6S265, which is a marker that is centromeric of HIA-A, in a telomeric direction through D6S276, a marker at which
                                                                                                                                                                                                                                                                                                                                                                              "G to A substitution (24d1 mutation associated with HH), results in Cys to Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This genomic DNA sequence corresponds to the human gene whose
                                                                                                                                                                                                                                                                                             /*tag= g
/note= "C to G substitution (24d2 mutation)
                                                                                                                                                                                                                                                                                                                                                   results in Ser to Cys substitution"
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"A to T substitution (24d7 variant)
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                                                                                                                 /*tag= a
/note= "contains introns"
                                                                                             cocation/Qualifiers
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96US-0630912.
96US-0632673.
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16-APR-1996;
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(first entry)

21-FEB-2001

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              critical in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in disease. This comprises a G to A substitution that is present in the end of the fill and the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in the results at C of Tyr substitution in the encoded protein (see AAW36499) at a critical disulphide bridge important for secondary is tructure. The following are claimed: the HH genemic DNA [1], a 1437 bp cDNA sequence (Ia) (see AAM36691) and their 24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method to determine the presence or absence of the common HH gene to determine the presence or absence of the common HH gene mutation; an annimal model for the HH disease; metal chelation agents for the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidation of injury due to oxidation of injury due to oxidation of the due of oxidation of the due of oxidation of the due of oxidation of the due of oxidation of the 
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A single mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18; Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the HH gene. The invention also relates to moverable for HH homozygotes, to HH diagnosis, prenatal screening and diagnosis, and therapies of HH disease, including gene therapy, protein- and antibody-based therapeutics, and small molecule
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0; Mismatches 1;
  allelic association was no longer observed.
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Matches 433; Conservative
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AAC68425 standard; DNA; 10825 BP.

AAC68425 RESULT

AAC68425

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10825;
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                                                                                                                                                                                                                                                                                                                    Tsuchihashi Z,
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.larity 99.8%; Pred. No. 3.5e-121;
Conservative 0; Mismatches 1;
                                                        HH; hereditary hemochromatosis; chelation agent; I-cell differentiation factor; iron overload; ds.
                                                                                                                                                                                                                                                                                                                      Ruddy D,
                           Human hereditary hemochromatosis DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 3; 108pp; English.
                                                                                                                                                                                                                              96US-0630912.
                                                                                                                                                                                               97US-0834497.
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96US-0652265.
                                                                                                                                                                                                                                                                                         (BIRA ) BIO-RAD LAB INC.
                                                                                                                                                                                                                                                                                                                      Thomas WJ, Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-006341/01.
P-PSDB; AAB36869.
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Matches 433; Conserv
                                                                                                                                                                                               04-APR-1997;
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                                                                                                        Homo sapiens
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23-MAY-1996;
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The present invention describes hereditary haemochromatosis gene products from the human haemochromatosis gene. The present sequence crepresents a hereditary haemochromatosis (HH). Also described is a unaffected by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely products for the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a RoRet gene which can be used to develop products for the study, diagnosis and
                                                                                                                                                                                                       GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965
241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
                                                                                 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; 8s.
                              TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGGCAATCAAAGGCTTTAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                         AAV57926 standard; DNA; 235033 BP.
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96US-0724394
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01-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
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99.8%; Pred. No. 3.5e-121;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                  Human hereditary hemochromatosis 24d2 mutation DNA
                                                                                                                                                                                                                                                                                                                          HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.
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                                                                                                                                                      BP.
                                                                                                                                                    AAC68427 standard; DNA; 10825
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96US-0632673.
96US-0652265.
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Conservative
                                              rirircigririae 6039
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                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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23-MAY-1996;
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nes 433;
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GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCCAGAGATATACGTGCCAGGTGGAGC 240
                                                                                                                             The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                        New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                Length 10825;
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                                                                                                                                                                                                                                      Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                               / Match 99.3%; Score 430.8; DB 22; Local Similarity 99.5%; Pred. No. 1.1e-120; nes 432; Conservative 0; Mismatches 2;
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                                                                                                     Disclosure; Fig 3; 108pp; English
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 2001-006341/01.
   WPI; 2001-006341,
P-PSDB; AAB36870
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      genes
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                                                                                                                     Gaps
                                                                                         DB 19; Length 235033;
                                                           235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;
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treatment of lupus and Sjogren's syndrome; and (2) NPT3 and which are homologues of a type 1 sodium transport gene, and similarly be used for hypophosphatemia.
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T-cell differentiation factor; iron overload; ds
                                                                                       Score 432.4; DB 19
Pred. No. 1.1e-120;
0; Mismatches 1;
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96US-0632673.
96US-0652265.
                                                                                       Query Match
Best Local Similarity 99.8%;
Matches 433; Conservative
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23-MAY-1996;
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Feder JN;
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                                                                                                                                                                                                                                      invention relates to hereditary hemochromatosis gene
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                                                                                                                                                                                                                                                                                                                   Sequence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 other;
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                                                                                                    Tsuchihashi
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Pred. No. 1.1e-120;
0; Mismatches 2;
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                                                                                                    Ruddy
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                                                                                                    Drayna DT, Gnirke A,
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96US-0632673.
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              97US-0834497
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                                                                                BIRA ) BIO-RAD LAB INC
                                                                                                                                       WPI; 2001-006341/01.
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es 432; Conserv
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               04-APR-1997;
                                    04-APR-1996;
16-APR-1996;
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                                                                                                      Thomas WJ,
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AAV57903/c ID AAV57903 standard; DNA; 237326 BP.

RESULT 10

AAV57903

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method to determine the presence or absence of the common hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of a haplotype or genotype where the presence of the haplotype genotype indicates the likely presence of the HFB gene mutation in the genomy of the individual. The HFB gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFB. The present invention also describes BFF genes which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a ROREt gene which are homologues of a type 1 sodium transport gene, and can can be used to develop.
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                                                                  Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis (HH) affected individual. Also described is a
Hereditary haemochromatosis subregion from an HH affected individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes hereditary haemochromatosis gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruddy DA,
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Conservative
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96US-0724394
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Tsuchihashi Z, Wolff
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16-APR-1996;
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11316 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 41257
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                                                                                       11256 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGGAGCCAGGA
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llarity 99.8%; Pred. No. 8.4e-117;
Conservative 0; Mismatches 1;
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96US-0652265.
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23-MAY-1996;
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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
RK;
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                                                                                                                                                                                        HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; 88.
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96US-0632673.
96US-0652265.
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                                                                               AAC68441 standard; DNA;
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membrane

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nucleic acid into a cell through its lipoprotein outer
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                                                                                                                                                   Similarity
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                                                                                                                                     Query Match
Best Local Simil
Matches 329; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hereditary hemochromatosis gene; encapsulate; lipoprotein outer membrane; membrane stability; test cell; molecular diagnosis; genetic testing; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a nucleic acid sequence that is used as a reference sequence to exemplify the method of the invention. The specification describes a method for the biological preparation of a stably encapsulated reference nucleic acid for molecular diagnostic and genetic testing. The method comprises inserting a vector containing a
                                                                                                                                                                                                                                                                                                                                                                               TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCCAATCAAAGGCTTTAACTT 418
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                                                      TGCCTCCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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                            ..
 DB 22; Length 517;
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                            Indels
Score 414.8; DB 22,
Pred. No. 2.6e-116;
0; Mismatches 2;
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 95.6%;
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                            Conservative
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                Local Similarity
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to encapsulate the nucleic acid, multiplying the cell to propagate the nucleic acid, inducing cell death without affecting the nucleic acid, and achieving a desired stability of the cell membrane for substantially matching the nucleic acid with the membrane stability of test cells. The reference nucleic acids are useful for molecular diagnosis and genetic
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                                                                                                                                                                                                                                                                                                                                                                                             GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                               Length 359;
                                                                                                                                                                                                                                                          0; · Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
                                                                                                                                                               Sequence 359 BP; 86 A; 91 C; 101 G; 81 T; 0 other;
                                                                                                                                                                                                          75.8%; Score 329; DB 20;
100.0%; Pred. No. 3.2e-90;
ive 0; Mismatches 0;
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14-APR-1998 (first entry)

AAT96691;

Laham N;

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The invention relates to a soluble polypeptide (I) of beta 2

microglobulin (beta2m)/HFE monochain comprising human beta2m (or its

microglobulin (beta2m)/HFE monochain comprising human beta2m (or its

malogue or active fragment). Linked to alphal-alphal domains of human

HFE (a central regulator of iron absorption; undefined) or its analogue

or active fragment, by a flexible linker peptide, or a functional

ederivative or salt of (I). (I) is useful for reducing intracellular iron

absorption in patients having hereditary haemochromatosis, transfusions,

thalassaemias, haemolytic anaemia or chronic infections, and for

chain barrier. (I) is further useful for treating transfusions,

cc delivering a therapeutic to cells that over-express transferrin receptor

(TfR) which are preferably lymphocytes or leukocytes, across the blood-

brain barrier. (I) is further useful for treating brain tumour. (I)

cc is also useful for treating oxidative stress disorders resulting in

ct issue damage e.g. vascular diseases, inflammation, atherosclerosis,

cut sommune diseases and inflammatory conditions. The monochain manifests

autoimmune diseases and inflammatory conditions. The monochain manifests

cs pecific characteristics advantageous for drug delivery systems. It is a

specific characteristics advantageous for drug delivery systems. It is a

csoluble, stable and fully conformed protein. It binds specifically to

cransferrin receptor (TfR) and therefore targets cells that over-express

cc slubling efficient drug delivery. It dissociates from the receptor,

cells, minimising side effects. It negatively regulates iron absorption,

reducing growth of undesired cells and preventing lymphocyte activation.

ccells, minimising side effects. It negatively regulates iron absorption,

reducing yrowth of undesired cells and preventing lymphocyte activation.

ccells, minimising side effects it is a self non-polymeric protein and delivery of

charges via monochain is expected to overcome drug-resistance since it is a

ccontacted to t
                                                                                                                                                                                             Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coding sequence of beta2m/HFE monochain.
                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 2; 77pp; English.
                                                           Ehrlich R, Rotem-Yehudar R,
                                                                                                               2002-383192/41
(MCIN/) MCINNIS P.
                                                                                                                                                                                                                                                                                                a linker peptide
                                                                                                                                           P-PSDB; AAU80035
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1013 ececritica Actracic con Garcar Carcar Garage Tecritica Actra Carcara 1072 1073 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1132 953 recerectriegicaadesteacararcardicaecerereagaecaereaecaecterae GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60 Gaps 0 Score 277; DB 24; Length 1317; Pred. No. 3.8e-74; 0; Indels Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other; Query Match 63.8%; Score 277; DB Best Local Similarity 100.0%; Pred. No. 3.8 Matches 277; Conservative 0; Mismatches 121 61 g g 셤 à à

181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGG 1229 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGG 277 1133 241 1193 ò ò

AAT96691 standard; cDNA; 1440 BP.

RESULT 15 AAT96691 ID AAT96

i "G to A substitution (24d1 mutation associated with HH), results in Cys to Tyr substitution" g co g substitution (24d2 mutation) results in His to Asp substitution" h "A to T substitution (24d7 variant) results in Ser to Cys substitution" Hereditary haemochromatosis; metal toxicity; diagnosis; Thomas WJ; Gnirke A, Ruddy D, Hereditary haemochromatosis gene cDNA clone gene therapy; prenatal screening; human; ss Location/Qualifiers 222.1268 (MERC-) MERCATOR GENETICS INC. 96US-0652265. 96US-0630912. 96US-0632673. 97WO-US06254 ď Drayna DT, Feder JN, Gn Tsuchihashi Z, Wolff RK; /*tag= /note= ' 1066 /*tag= /note= ' /*tag= 408 /*tag= /note= 414 04-APR-1997; 23-MAY-1996; 04-APR-1996; 16-APR-1996; sapiens WO9738137-A1 16-0CT-1997. variation mutation mutation Homo

Hereditary haemochromatosis gene and variants - useful for diagnosis and treatment of hereditary haemochromatosis disease P-PSDB; AAW36499

WPI; 1997-512743/47.

This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmid-based cDNA library following identification of the HH locus in the HLA region of chromosome . A single mutation (24d1) in the HH gene responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a chromism and in the encoded protein (see AM36499) at a critical disulphide bridge important for secondary structure. The following are claimed: a 10825 bp genomic DNA sequence (I) (see following are claimed: a 10825 bp genomic DNA sequence (I) (see following are claimed: a cloning or expression vector; host cells; a special product chosen from the HH gene product, its variants credices for the HH gene product chosen from the HH gene product is search and 24d7, 24d2 and 24d7, or a peptide of at least 56 amino acid residues of these sence or absence of the common HH gene condetermine the presence or absence of the common HH gene condetermine the presence or absence of the common HH gene condetermine the presence or absence of the common HH gene mutation; an annimal medal for the HH disease; metal agents for the mitigation of injury due to oxidative process in vivo or mitigation of iron overload; a method for screening potential Disclosure; Fig 4; 115pp; English.

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958 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1017
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therapeutic agents for activity in connection with HH disease, an antisense oligonucleotide directed against a transcriptional product of anucleic acid sequence as above, and oligonucleotides or pairs of oligonucleotides covering a range of nucleotides from (I), (Ia) or their variants, useful for detecting a polymorphism in the HH gene. The invention also relates to methods for screening for HH homozygotes, to HH diagnosis, prenatal screening and diagnosis, and therapies of HH disease, including gene therapy, protein—and antibody-based therapeutics, and small molecule
                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                  63.6%; Score 276; DB 18; Length 1440; 100.0%; Pred. No. 7.9e-74; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                         Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;
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Matches 276; Conservative
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cgn2 6/ptodata/1/pubpna/DCT_NEW_PUB.seq:*
cgn2 6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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cgn2 6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
cgn2 6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                             OM nucleic - nucleic search, using sw model
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 27, Appl	Sequence 3112, Ap		GENERAL INFORMA	GENERAL INFORMA	GENERAL INFORMA	Sequence 1, Appli	GENERAL INFORMA	GENERAL INFORMA	Sequence 2, Appli	Sequence 20, Appl	Sequence 21, Appl	Sequence 9, Appli	Sequence 11, Appl	Sequence 77, Appl
SUMMARIES	ID	US-09-981-606-27	US-09-764-877-3112	US-10-242-515-3112	US-10-138-888-1	US-10-138-888-5	US-10-138-888-79	US-10-301-844-1	US-10-138-888-3	US-10-138-888-7	US-10-301-844-2	US-10-138-888-20	US-10-138-888-21	US-10-138-888-9	US-10-138-888-11	US-10-138-888-77
	1	13	10	12	13	13	13	15	13	13	15	13	13	13	13	13
	% Query Match Length DB	12146	5749	5749	10825	10825	10825	235033	10825	10825	237326	517	517	1440	1440	1440
	% Query Match	100.0	99.6	99.6	99.66	9.66	9.66	9.66	99.3	99.3	99.3	95.9	95.6	63.6	63.6	63.6
	Score	434	432.4	432.4	432.4	432.4	432.4	432.4	430.8	430.8	430.8	416.4	414.8	276	276	276
	Result No.	7	7	m	4	Ŋ	9	0 7	00	σ	c 10	11	12	13	14	15

Seguence 1, Appli	Sequence 10, Appl	Sequence 12, Appl	112	o,	'n	Sequence 112, App	113,	113,	113,	113			Sequence 6712, Ap				Sequence 2302, Ap	Sequence 351, App	383,	Sequence 19081, A		11,	Sequence 5325, Ap	Sequence 350, App	Sequence 4806, Ap		325		Sequence 563, App
US-09-981-606-1	US-10-138-888-10	US-10-138-888-12	US-10-272-665-112	US-10-273-321-112	US-10-272-756-112	US-10-273-228-112	US-10-272-665-113	US-10-273-321-113	US-10-272-756-113	US-10-273-228-113	US-10-029-386-18154	US-10-029-386-4454	US-09-764-891-6712	US-10-091-572-573	US-09-880-107-3713	US-10-029-386-5014	US-10-029-386-2302	US-10-158-057-351	US-10-158-057-383	US-10-029-386-19081	US-09-864-761-21544	US-09-962-436-311	US-10-029-386-5325	US-10-158-057-350	US-09-864-761-4806	US-10-029-386-18770	US-09-918-995-32571	US-10-093-463-77	US-10-044-090-563
13	13	13	13	13	13	13	13	13	13	13	13	13	11	12	10	13	13	12	12	13	σ	σ	13	12	Φ	13	11	13	14
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63.6	63.2	63.2	21.4	21.4	21.4	21.4	21.1	21.1	21,1	21.1	20.3	20.3	20.3	20.3	19.9	19.6	19.6	19.6	19.6	19.3	19.3	19.3	19.3	19.3	19.2	18.8	18.8	18.8	18.8
276	274.4	274.4	93	69	93	93	91.4	91.4	91.4	91.4	88	88	88	88	86.4	85.2	85.2	85.2	85.2	83.6	83.6	83.6	83.6	83.6	83.2	ä	81.8	81.8	81.8
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	c 33	34	35	36	ι'n	38	c 39	40	n 41	42	43	44	45

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                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 434; DB 13; Length 12146; 100.0%; Pred. No. 8.3e-139;
                                                                  APPLICANT: Rothenberg et al.
TITLE OF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
              ; Sequence 27, Application US/09981606; Publication No. US20030129595A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 434; Conservative
                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                        LENGTH: 12146
US-09-981-606-27
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OTHER INFORMATION: n equals a,t,g, or
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Publication No. US20040009488A1
GENERAL INFORMATION:
                  421 TITTCTGTTTTAG 434
                                                    2025 TTTTCTGTTTTAG
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NAME/KEY: misc feature
LOCATION: (1222)
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                                                                                                                   RESULT 3
US-10-242-515-3112
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5674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
                                                                 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA
                                         ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGATGAGCCAGGA
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3112
LENGTH: 5749
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Pred. No. 2.1e-138;
0; Mismatches 1;
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COTHER INFORMATION: n equals a,t,g, or US-09-764-877-3112
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3112, Application US/09764877; Patent No. US20020147140A1; GENERAL INFORMATION:
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Best Local Similarity 99.8
Matches 433; Conservative
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US-09-764-877-3112
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1725 IGGAIGCCAAGGAGITCGAACCTAAAGACGIAIIGCCCAAIGGGGAIGGGACCTACCAGG 1784
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies PITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC005C1; FILE REFERENCE: PC005C1; FILE REFERENCE: PC005C1; FILE REFERENCE: PC005C1; FILE REFERENCE: PC005C1; FILE REFERENCE: PC005C2-09-13; PRIOR PELICATION NUMBER: 09/764,877; PRIOR FILING DATE: 2000-01-31; PRIOR FILING DATE: 2000-01-31; PRIOR FILING DATE: 2000-00-131; PRIOR FILING DATE: 2000-00-01-31; PRIOR PILING DATE: 2000-00-06-28; PRIOR PELICATION NUMBER: 60/217,487; PRIOR PELICATION NUMBER: 60/225,758; PRIOR PELICATION NUMBER: 60/225,758; PRIOR PELICATION NUMBER: 60/225,758; PRIOR PELICATION NUMBER: 60/225,963; PRIOR PELICATION NUMBER: 60/220,963; PRIOR PELICATION NUMBER: 60/225,447; PRIOR PELICATION NUMBER: 60/225,447; PRIOR APPLICATION NUMBER: 60/225,447; PRIOR PELICATION NUMBER: 60/225,447; PRIOR PELICATION NUMBER: 60/213,496; PRIOR PELICATION NUMBER: 60/218,290; PRIOR PELICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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99.6%; Score 432.4; DB 12;
Best Local Similarity 99.8%; Pred. No. 2.1e-138;
Matches 433; Conservative 0; Mismatches 1;
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5606 TGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                   Length 10825;
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                   NAME/KEY: allele
LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                                                                                                                                         99.6%; Score 432.4; DB 13 ilarity 99.8%; Pred. No. 2.8e-138; Conservative 0; Mismatches 1;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Amer
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                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO:
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
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/label= 24d7
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                          Matches 433;
                                                                                                                                                                                                                                               US-10-138-888-1
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                                                                                                                              420
                                                                                                                              TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGCTGGCAATCAAAGGCTTTAACTTGC
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TELEFAX: (212) 869-8864
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "No. US20030148972A1mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
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OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
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COMPUTER: 1BM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
FILING DATE: 04-APR-1996
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CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.
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                                                                                                                                                                                                                                                         TTTTTCTGTTTTAG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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5905

Orayna, Dennis T.

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5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785
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Pred. No. 2.8e-138;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Hereditary Hemochromatosis (HH)
                                                                                                                                                                                                                                                   NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
FILING DATE: 02-May-2002
CLASSIFICATION: UDKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) LOCATION: 5507..6023
) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-138-888-5
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Best Local Similarity 99.8%;
Matches 433; Conservative
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.

RESULT 6 US-10-138-888-79

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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                              Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /product= "Hereditary (HH) protein containing the 24d7 mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.6%; Score 432.4; DB 13
99.8%; Pred. No. 2.8e-138;
iive 0; Mismatches 1;
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION NUMBER: US/80/136,888
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,265
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Hereditary Hemochromatosis
(HH)gene 24d7 allele"
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US-10-138-888-79
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-8864
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Best Local Similarity 99.8
Matches 433; Conservative
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                                                                         GGGCCTTGAACTACCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCAA 120
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TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                               41484 GGGCCTTGAACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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Frefer, John N.
Gnirke, Andreas
Ruddy, David
Tsuchinhashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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APPLICATION NUMBER: US 08/634,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
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NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
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; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
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CORRESPONDENCE ADDRESS:
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        TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ruddy, David A.
Wolff, Roger K.
TITLE OF INVENTION: PLOLYMORPHISMS IN THE REGION OF THE HUMAN
HENOCHROMATOSIS GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBW PC compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSEO for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/301,844

FILING DATE: 20-No. US20030100747A1-2002

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 432.4; DB 15;
Pred. No. 1e-137;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
TELEPRONE: 650-493-4935
TELEFRAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
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LENGTH: 235033 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10301844 Publication No. US20030100747A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 99.8%;
Matches 433; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               421 TTTTTCTGTTTTAG 434
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FEATURE:
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                                             (HH) protein containing the 24d1
                                                                                                                                                                                                                                                                                                                                       Score 430.8; DB 13; Length 10825; Pred. No. 1e-137; 0; Mismatches 2; Indels 0;
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Feder, John N.
Fener, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                             /note= "Hereditary Hemochromatosis (HH)
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                       Query Match 99.3%; Score 430.8; Best Local Similarity 99.5%; Pred. No. 1e-1 Matches 432; Conservative 0; Mismatches
                                                                                                                                                                                                                                                            LOCATION: 5507..6023
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                 TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
OTHER INFORMATION: /produ
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US-10-138-868-7
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
--dar. John B.
                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                          NAME/KEY: -
LOCATION: 140..7319
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STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                   FEATURE
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFEREATION NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRAX: (212) 869-8864
OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing both the 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 10825;
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ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and 24d2 mutations"
/note="Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/62,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                    APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                         CURRENT APPLICATION DATA:
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41316 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGATATACGTACCAGGTGGAGC 41257
                                                                                                                                41256 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGGGGCCAGGA 41197
                                                                                                                                                                                                                    41196 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 41137
                                                                                                                                                                                                                                                                                                   41136 TGAGGATCTGCTCTTTGTTAGGGGTGGGCTGGGGGGGGCAATCAAAGGCTTTAACTTGC 41077
    GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
                                                                                                                                                                           GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA
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Ruddy, David
Tuddy, David
Tudhihashi, Zenta
Wolff, Roger K.
TILE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FLING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/10138888
Publication No. US20030148972A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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US-10-138-888-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41376 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 41317
5906 GCTGAGAAARTCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965
                                               420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ruddy, David A. Wolff, Roger K. TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15; Length 237326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.3%; Score 430.8; DB 15
99.5%; Pred. No. 3.8e-137;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPRAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                HEMOCHROMATOSIS GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-301-844-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 237326 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             Sequence 2, Application US/10301844 Publication No. US20030100747A1 GENERAL INFORMATION:
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                                                                                                                                                       5026 TTTTCTGTTTAG 6039
                                                                                                                                TTTTTCTGTTTTAG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                             TGAGGATCTGCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NY
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Matches 432;
                                          361
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: -
LOCATION: 1..517
OTHER INFORMATION:
                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 416; Conserv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTT 418
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                                                                                  /note= "normal or wild-type (unaffected)
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                    Length 517;
                                                                                                                                                                                                                  LOCATION: replace (328, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
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Publication No. US20030148972A1

GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.

Feder, John N.

Gnirke, Andreas

Ruddy, David

TSuchihashi, Zenta

Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                          NAME/KET: . LOCATION: 1.517
COTHER INFORMATION: /note= "normal or wild genomic sequence surrounding variant for 2441(G) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (SEQ ID NO:1)"
                                                                                                                                                                                                                                                                                                                                                                    DB 13;
                                                                                                                                                                                                                                                                                                                                                                95.9%; Score 416.4; DB 13 99.8%; Pred. No. 2.6e-133; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                   /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                   NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                        NAME/KEY
                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                          JS-10-138-888-20
                                                                                                                                                                                                                                                                                                                                                                                                        417;
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US-10-138-888-21
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: replace(328, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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  Version #1.30
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al Similarity 99.5%; Pred. No. 9.4e-133;
416; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /note= "genomic seque
variant for 24d1(A) allele corresponding
to positions 5507-6023 of genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                         APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
FILING DATE: 16-APR-1996
FILING DATE: 04-APR-1996
                       CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKnown>
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence containing the HH gene (SEQ ID NO:3) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLGCY: linear
MOLECULE TYPE: DNA (genomic)
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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1018 GCTGGATRACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                  838 TGCCTCCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            898 GGGCCTTGAACTACTCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GGGCCTTGAACTACTCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                              NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
              OTHER INFORMATION: /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                        Length 1440;
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Feder, John N.
Gnirk, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DAIA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 276
                                                                                                                                                                                                                                                                                 63.6%; Score 276; DB 13;
100.0%; Pred. No. 1.4e-84;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICATION NUMBER: US/10/136,888
FILING DATE: 02-May-2002
CLASSIPICATION: «UDKNOWN»
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/634,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
APPLICATION NUMBER: US 08/652,655
FILING DATE: 23-MAX-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/10138888
Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: USA
                                                                                                                                                                    (unaffected) "
                                     (unaffected)
(label= 24d7
                                                                                                                                                                                              label= 24d1
                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-138-888-11
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400 GCTGAGAAATCTATTGGGGTTGAGAGGGGTGCCTGAGGAGGTAATTATGGCAGTGAGA 459
                                                                 361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGCTGGCAATCAAAGGCTTTAACTT 418
                                                                                                                 460 rdaddarcrecrerrationaddddardddarddaarcaarcaaacerraacri 517
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OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFFRARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace(414, "a")
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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                                                                                                                                                                                                                      Sequence 9, Application US/10138888
Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
222..1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: (212) 869-
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
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COUNTRY: USA
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LOCATION:
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US-10-138-888-9
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Search completed: February 11, 2004, 21:02:46 Job time : 274.96 secs
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OTHER INFORMATION: /phenotype= "Hereditary HemochromatoBis
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Preder, John N.
Galrke, Andreas
Ruddy, David
Truch, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1078 ACCCAGGCCTGGATCAGCCCTCATTGTGATCTGGG 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.6%; Score 276; DB 13; Best Local Similarity 100.0%; Pred. No. 1.4e-84; Matches 276; Conservative 0; Mismatches 0;
                                                                                      NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= 24d2
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 77, Application US/10138888
Publication No. US20030148972A1
                                                                                                                                                                                                                                                                        LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
222..1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA
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LOCATION:
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US-10-138-888-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           838 IGCCTCCTTIGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 897
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compastible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1078 Acccadeccredarcaeccccrcarrergarcress 1113
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63.6%; Score 276; UB 13.;
Best Local Similarity 100.0%; Pred. No. 1.4e-84;
Matches 276; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brian M. Poissant
REGISTRATION UNDBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                 FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/10/138,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 77:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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STRANDEDNESS: single
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Run on:

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4: /cgn2 6/ptodata/1/pna/USO8_COMB.seq:*
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14: /cgn2 6/ptodata/1/pna/USO9_COMB.seq:*
15: /cgn2 6/ptodata/1/pna/USO9_SA_COMB.seq:*
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18: /cgn2 6/ptodata/1/pna/USO9_SA_COMB.seq:*
19: /cgn2 6/p
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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pna/US6032_COMB.seq:
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pna/US6034_COMB.seq:
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pna/US6037_COMB.seq:
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101:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli Sequence 1, Appli Sequence 27, Appli Sequence 18070, A
ΩI	SU SU SU SU SU
98	21 21 32 32
% Query Match Length DB	434 100.0 12146 21 434 100.0 12146 21 434 100.0 12146 43 2.4 99.6 2555 32
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Sequence 12922, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 51931, A
Sequence 85138, A
Sequence 3, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
GENERAL INFORMA
                                            Sequence 3112, Ap
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Sequence 112, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
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GENERAL INFORMA
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Sequence 18072,
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GENERAL INFORMATION:
GENERAL INFORMATION:
TATLE OF INVENTION:
FILE REPERENCE: 476-98/PAR
CURRENT APPLICATION NUMBER: US/09/439,378
CURRENT APPLICATION NUMBER: 2,272,410
FRIOR APPLICATION NUMBER: 2,272,410
FRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE PRESENCE: APPLICATION VERY CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTR
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Pred. No. 2.7e-117;
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US-10-138-888-7
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US-08-852-495C-2
US-08-894-497-20
US-08-891-250-3
US-08-891-250-3
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ORGANISM: Homo sapiens
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LENGTH: 12146
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TILLS OF INVENTION: METHOD FOR DIAGNOSIS OF HEREDITARY HEMOCHROMATOSIS
FILE REFERENCE: 4767-98/PAR
CURRENT APPLICATION NUMBER: US/09/439,378A
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: 2,272,410
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 8
SEG ID NO: 1
LENGTH: 12146
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100.0%; Score 434; DB 21;
Best Local Similarity 100.0%; Pred. No. 2.7e-117;
Matches 434; Conservative 0; Mismatches 0;
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CRGANISM: Homo sapiens
US-09-439-378A-1
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US-09-439-378A-1
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TITLE OF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR PILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 27
                                                                                                                                                                                                                      Sequence 27, Application US/09981606
GENERAL INFORMATION:
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Matches 434; Conservative
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US-09-981-606-27
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US-09-724-676-18070
Sequence 18070, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD

RESULT 4

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Pred. No. 4.7e-117;
0; Mismatches 1; Indels 0;
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TITLE OF INVENTION: Variants of alternative splicing FILE REFERRICE: 129181.4 Compugen CURRENT PEPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO 18070 LENGTH: 2555
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Pred. No. 4.7e-117;
0; Mismatches 1;
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TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181-4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ:ID NO 18070
LENGTH: 2555
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Matches 433; Conservative
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Best Local Similarity 99.8
Matches 433; Conservative
                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-724-676-18070
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ORGANISM: Homo sapiens
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US-09-724-676A-18070
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Sequence 3112, Application PC/TUS0101338
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005PCT
CURRENT APPLICATION NUMBER: PCT/US01/01338
                                                                                                                                                                                                                                                                                                                                                                                             Score 432.4; DB 32
Pred. No. 4.8e-117;
0; Mismatches 1;
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Best Local Similarity 99.8%;
Matches 433; Conservative
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ORGANISM: Homo sapiens
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                                                        TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAAGG 180
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                      GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVERTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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99.6%; Score 432.4; DB 35
Best Local Similarity 99.8%; Pred. No. 4.8e-117,
Matches 433; Conservative 0; Mismatches 1,
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ORGANISM: Homo Bapiens
US-09-724-676-18073
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US-09-724-676-18073
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LENGTH: 2819
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TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 4031 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3112 INOTER OF SEQ ID NO 3112
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005PCT
CURRENT APPLICATION NUMBER: PCT/US01/01338
CURRENT FILING DATE: 2001-01-14
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 403.
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 6.2e-117;
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CTHER INFORMATION: n equals a,t,g, or PCT-US01-01338-3112
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CCATION: (1222)
OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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Best Local Similarity
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PCT-US01-01338-3112
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           Length 5749;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3112
LENGTH: 5749
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     Score 432.4; DB 2;
Pred. No. 6.2e-117;
0; Mismatches 1;
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COTHER INFORMATION: n equals a,t,g, or US-09-764-877-3112
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Query Match
Best Local Similarity 99.8'
Matches 433; Conservative
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433; Conservative
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US-09-764-877-3112
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Best Local S:
Matches 433,
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1665 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 1724
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APPLICATION NUMBER: US/08/634,497
FILING DATE: 04-APR.1997
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR.1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR.1996
CLASSIFICATION NUMBER: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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FILING DATE: 04-APR-1996
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APPLICANT: Draya, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Heady, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
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ATTORNEY AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y: USA
94111-3834
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CLASSIFICATION:
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                                                                                               1785 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
                                                                                                                                                 241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC005C1
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
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Pred. No. 6.2e-117;
0; Mismatches 1;
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PRIOR FILING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-31
PRIOR PLING DATE: 2000-01-31
PRIOR PLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/19,628
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR PILING DATE: 2000-06-18
PRIOR PILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3112, Application US/10242515; GENERAL INFORMATION:
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Best Local Similarity 99.8%;
Matches 433; Conservative (
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ORGANISM: Homo sapiens
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5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785
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                                                                                                                     181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
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APPLICANT: Thomas, Winston J.
APPLICANT: Peder, John N.
APPLICANT: Galirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Reger K.
APPLICANT: Wolff, Reger K.
APPLICANT: Wolff, Reger K.
NUMBER OF SEQUENCES: 76
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 33-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION 135
PRIOR APPLICATION WHERE: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION WHERE: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLI
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
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TELEFRAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-196
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2 (C) OTHER INFORMATION: allele (SEQ ID NO:41)" allele (SEQ ID NO:20); correctly other information: normal or wild-type (unaffected) genomic OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: allele (SEQ ID NO:20); correctly other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); and other information: allele (SEQ ID NO:20); 
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                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "Normal or wild-type (unaffected) OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION; allele"
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(unaffected)"
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(unaffected)"
/label= 24d7
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/label= 24d1
REFERENCE/DOCKET NUMBER: 017957-000520US TELEOPHONE: (650) 326-2400
TELEPHONE: (650) 326-2422
INFORMATION FOR SEQ ID NO: 1: SRQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
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NAME/KEY: allele
LOCATION: replace(3872, "C")
OTHER INFORMATION: (unaffected)
OTHER INFORMATION: (label= 24d,
FEATURE:
NAME/KEY: allele
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CTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: /label= 24
FEAUTRE:
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OTHER INFORMATION: (unaffecte
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: /label= 2.
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Matches 433; Conservative
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NAME/KEY: -
LOCATION: 140..7319
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NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
OTHER INFORMATION:
                                                                                                                                                                                                                                                  APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Normal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
allele"
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC computatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,957
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/834,497
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 13-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION DATE: 16-APP-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APP-1996
FILING DATE: 16-APP-1996
FILING DATE: 04-APP-1996
ATTORNEY AGENT THORNATION:
ANDARY AGENT THORNATION:
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMOUNICATION INFORMATION:
TELEFAX: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 650-493-556
IELERAX: 650-493-556
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                       Sequence 1, Application US/09497957
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
           6026 TTTTCTGTTTTAG 6039
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 Av.
CITY: New York
STATE: New York
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                                                                                                                   RESULT 14
US-09-497-957-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5966 TGAGGATCTGCTCTTTGTTAGGGGGGGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGGCCTTGAACTACTACCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGGCCAGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.6%; Score 412.4; DB 13; Length 10825; Best Local Similarity 99.8%; Pred. No. 7.6e-117; Matches 433; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                NAME/KEY: CDS
IOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation."
OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene 24d2 allele"
NAME/KEY: -
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20) "

FRATURE: // NAME/KEY: allele (SEQ ID NO:20) "

COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis of OTHER INFORMATION: /label= 24d2

US-08-834-497-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: 3852..3891
OCTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
NAME/KEY: .
                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 5, Application US/09497957 GENERAL INFORMATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5786 GCTGGATAACCTTGGCTGTACCCCCTGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.6%; Score 432.4; DB 21; Length 10825; Best Local Similarity 99.8%; Pred. No. 7.6e-117; Matches 433; Conservative 0; Mismatches 1; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                        /note= "start and stop positions for
normal or wild-type (unaffected) genomic
sequence surrounding variant for 24d2(C)
allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "start and stop positions for
normal or wild-type (unaffected) genomic
sequence surrounding variant for 24d1(G)
allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: allele
LOCATION: replace (1872, "c")
OTHER INFORMATION: (unaffected) "
OTHER INFORMATION: /label= 24d2
FEATURE:
NAME/KEY: allele
LOCATION: replace (1878, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /label= 24d7
OTHER INFORMATION: /label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: replace(5834, "g")
OTHER INFORMATION: 'phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
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    CDNA (SEQ ID NO:9)"
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                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
LOCATION: 5507.6023
OTHER INFORMATION: /no
OTHER INFORMATION: seq
OTHER INFORMATION: seq
OTHER INFORMATION: seq
                                                                          NAME/KEY: -
LOCATION: 3852..3891
OTHER INFORMATION: no
OTHER INFORMATION: seconTHER INFORMATION: seconTHER INFORMATION: seconTHER INFORMATION: selection allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocations allocatio
OTHER INFORMATION:
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RESULT 15

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NAME/KRY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: //product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation"
OTHER INFORMATION: //note= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene 24d2 allele"
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Galirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: HERBITANY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
ADDITIONAL ADDRESS:
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OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: genomic sequence surrounding variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CORRATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,957
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILLING DATA:
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US/08/834,497
FILLING DATE: 0.4-APR-1997
APPLICATION NUMBER: US 08/652,265
FILLING DATE: 23-MAY-1996
FILLING DATE: 16-APR-1996
FILLING DATE: 16-APR-1996
FILLING DATE: 16-APR-1996
FILLING DATE: 04-APR-1996
ATJORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/630,912
FILLING DATE: 04-APR-1996
ATJORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,462
ATJORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELLEFAX: 650-493-4935
TELLEFAX: 650-493-556
TELLEFAX: 66141 PENNIE
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1155 Avenue of the Americas
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MOLECULE TYPE: DNA (genomic)
FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: single
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New York
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5606 TGCCTCCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665
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           FEATURE:

NAME/KEY:

LOCATION: 5507..6023

JOCATION: 5507..6023

OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"

FRATURE:

NAME/KEY:

COTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"

FRATURE:

NAME/KEY:

LOCATION: replace(3872, "g")

OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis

OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis

OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                                                                                                  Query Match
99.6%; Score 432.4; DB 21; Length 10825;
Best Local Similarity 99.8%; Pred. No. 7.6e-117;
Matches 433; Conservative 0; Mismatches 1; Indels 0;
OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
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Search completed: February 11, 2004, 18:19:20 Job time: 2491.59 secs

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ORGANISM: Homo Sapiens
US-09-277-457-27
SEQ ID NO 27
LENGTH: 12146
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  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
  /cgn2_6/ptodata/1/ina/PacKfiles1.seq:*
         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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3 US-08-679-729-27

3 US-08-652-265-1

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3 US-08-63-447-1

3 US-08-63-447-1

3 US-08-63-4447-20

US-08-672-3947-20

US-08-724-3947-20

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                                                                                                                                                                       569978 seqs, 220691566 residues
                                                                                                      6494 6927
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                                               nucleic search, using
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Match Length DB
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Patent No. 6355425
GENERAL INFORMATION:
APPLICANT: Rothenberg, Barry B.
APPLICANT: Barda-Hirai, Ritsuko
APPLICANT: Barton, James C.
ITLLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
FILE REFERENCE: 10653/00201
CURRENT APPLICATION NUMBER: US/09/277,457
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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Similarity 100.0%; Pred. No. 1.1e-141;
14; Conservative 0; Mismatches 0;
US-08-652-265-9

US-08-652-265-11

US-08-834-497A-9

US-08-834-447A-11

US-09-503-444A-11

US-09-577-457-1

US-09-577-457-1

US-09-679-729-1

US-08-652-265-12

US-08-834-497A-12

US-08-834-497A-12

US-08-834-447A-12

US-08-814-437A-12

US-09-503-444A-12

US-09-503-444A-12

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US-09-14-372C-3

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                                                                                                                                                             Sequence 27, Application US/09679729

Fatent No. 6509442

GENERAL INFORMATION:
APPLICANT: Rothenberg, Barry E.
APPLICANT: Sawada-Hirai, Ritsuko
APPLICANT: Barton, James C.
TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
FILE REFERENCE: 24065-1004 DIV
CURRENT APPLICATION NUMBER: US/09/679,729
CURRENT APPLICATION NUMBER: 09/277,457

PRIOR APPLICATION NUMBER: 09/277,457

PRIOR FILING DATE: 1009-03-26

NUMBER OF SEQ ID NOS: 30

SOFTWARE FAREST FAREST FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 414; DB 4; Length 12146; 100.0%; Pred. No. 1.1e-141; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
                                                           421 TITITCTGTTTTAG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rrrrrcrerrrad 6927
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Best Local Similarity 100.
Matches 434; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 27
LENGTH: 12146
                                                                                                                               RESULT 2
US-09-679-729-27
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/note= "No. 6025130mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
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LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2 (C) OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24d1(G) allele (SEQ ID NO:20)"
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: CDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..56
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: replace(3872, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
APPLICANT: Feder, John N.
APPLICANT: Ghirke, Andreas
APPLICANT: Guddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE PATENTIN Release #1.0, Version #1.30
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY 1996
CLASSIFICATION: 514
ATTOKNEY/AGENT INPOMATION:
NAME: SMITH, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/POCKET NUMBER: 17957-000500
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                   ZIP. 94111.3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION:
INFORMATION:
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OTHER INFORMATION:
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INFORMATION
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COMPUTER:
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                                                                                                                                                                                                                                                                                                                      Gaps
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                    NAME/KEY: allele
LOCATION: replace(5834, "g")
OTHER INFORMATION: 'phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                         /phenotype= "normal or wild-type
(unaffected)"
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Two Embarcadero Center, Eighth Floor
               LOCATION: replace (3878, "a")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: /label= 24
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Patent No. 6025130
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Best Local Similarity 99.8
Matches 433; Conservative
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NAME/KEY:
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US-08-652-265-1
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US-08-652-265-5
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ZIP: 94111-3834 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

CITY: San Francisco STATE: California

COUNTRY:

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2665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
OTHER INFORMATION: mutation" mutation: mutation "Hereditary Hemochromatosis (HH)
OTHER INFORMATION: gene 24d2 allele"
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LOCATION: replace(3872, "g")

OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 24d2
US-08-652-265-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: 3852..3891

LOCHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: genomic sequence surrounding variant
OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"
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                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23.MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
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Pred. No. 3.6e-141;
                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 37,23
REFERENCE/DOCKET NUMBER: 17957-000500
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
99.6%; Score 432.4;
Best Local Similarity 99.8%; Pred. No. 3.6e
Matches 433; Conservative 0; Mismatches
                             PC-DOS/MS-DOS
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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NAME/KEY: -
NAME/KEY: -
140..7319
                                                                                                                        FILING DATE: 23
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241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
                                                                                                                                                                                                         /note= "No. 6140305mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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                                                                                                               join(361..436, 3762..4025, 4235..4510, 5606..5881, 6040..6153, 7107..7147)
RMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: -
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) OTHER INFORMATION: allele (SEQ ID NO.41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24dl(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.6%; Score 432.4; DB 3; Length 10825; 99.8%; Pred. No. 3.6e-141;
                                                                                                                                                                                                                                                                                                                                        /note= "start and stop positions for
normal or wild-type (unaffected) allele
cDNA (SEQ_ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /phenotype= "normal or wild-type (unaffected)"
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(unaffected) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= 24d2
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                                                     MOLECULE TYPE: DNA (genomic)
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NAME/KEY:
LOCATION: 5507..6023
OTHER INPORMATION:
OTHER INPORMATION:
OTHER INPORMATION: 84
OTHER INFORMATION: 84
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Best Local Similarity 99.8
Matches 433; Conservative
                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION: 140.7319
OTHER INFORMATION: /
OTHER INFORMATION: C
FRATURE:
               single
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                                                                                                                  LOCATION: join (361.
LOCATION: 6040..615.
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
NAME/KEY: allele
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NAME/KEY: allele
LOCATION: replace
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FEATURE:
NAME/KEY: allele
             STRANDEDNESS:
                                                                                                NAME/KEY:
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5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845
                                                                                                                                                                     5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965
                                                                                                                                                                                                                                                          5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGGGGTGGCAATCAAAGGCTTTAACTTGC 6025
                                                                                                                             GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
                                                                                                                                                                                                               TGAGGATCTGCTCTTTGTTAGGGGATGGCTGGGTGGCAATCAAAGGCTTTAACTTGC 420
                                            241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
                                                                                       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows 95
SOFTWARE: FASTED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
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APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 9907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION WIMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08834497A Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: WEREDITARY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                    421 TITITCIGITITAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-834-497A-1
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STATE:
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                                      NAME/KEY: CDS
NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: ford.
LOCATION: ford.
COTHER INFORMATION:
OTHER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
99.6%; Score 432.4; DB 3; Length 10825;
Best Local Similarity 99.8%; Pred. No. 3.6e-141;
Matches 433; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: replace (3872, "g")

COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d2

US-08-834-497A-5
                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COTHER INFORMATION: for genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "start and stop positions for genomic sequence surrounding variant for 24d2(G) allele (SEQ ID NO:42)"
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LOCATION: 3852..3891
COTHER INFORMATION: /
COTHER INFORMATION: GEN
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NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: -
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US-09-503-444A-1
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5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGAGACCAGGA 5905
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                                                                                                      301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HERBIITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Pennie & Edmonds LI.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows 95
SOFTWARE: FESTEED for Windows Version 2.0b
CURRENT APPLICATION DATA:
PELLION NUMBER: US/08/834,497A
FILING DATE: 04-AFR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, BITCAN M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMUNICATION INFORMATION:
TELEFAX: 660-493-4935
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION: 514
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/630,912
PILING DATE: 04-APR-1996
CLASSIFICATION: 514
CLASSIFICATION: 514
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-834-497A-5
; Sequence 5, Application US/08834497A
; Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                  6026 TTTTTCTCTTTTAG 6039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                               421 TITITICIGITITAG 434
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Thomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 AV
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04
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OTHER INFORMATION: allele (SEQ ID NO:41)"
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Parent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Peder, John N.
APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: replace (5834, "g")
OTHER INPORMATION: (Unafferorype
OTHER INFORMATION: (Labele 24)
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Best Local Similarity 99.8<sup>7</sup>
Matches 433; Conservative
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Hereditary Hemochromatosis (HH) gene
allele"
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "No. 6228594mal or wild-type (unaf OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 3852.3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: CDNA (SEQ ID NO:9)"
                                                            APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuckhiasshi, Zenta
APPLICANT: Tsuckhiasshi, Zenta
APPLICANT: Tsuckhiasshi, Zenta
APPLICANT: Horditary Hemochromatosis Gene
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
TORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8907-0088-999
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SOFTWARE:
WordPerfect Version B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
FILING DATE: 23-May-1996
FILING DATE: 13-May-1996
PRIOR APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
RICH RAPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATORNEY/AGRNT INFORMATION:
NAME: POSISBAIL, BILAN M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-95
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
Sequence 1, Application US/09503444A
Patent No. 6228594
                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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- 3852..3891
                                             GENERAL INFORMATION:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGATGTGATGAGGGCAGGA 5905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5966 TGAGGAICTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGGCCTTGAACTACCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 IGGAIGCCAAGGAGTICGAACCIAAAGACGIATIGCCCAAIGGGGAIGGGACCIACCAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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                                                                                             /note= "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10825;
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/label= 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /phenotype= "normal or wild-type
(unaffected)"
/label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /phenotype= "normal or wild-type (unaffected)"
/label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.6%; Score 432.4; DB 3; 99.8%; Pred. No. 3.6e-141; cive 0; Mismatches 1;
PEATURE:
NAME/KEY:
LOCATION: 5507.6023
OTHER INFORMATION: /note= "star OTHER INFORMATION: normal or will other information: other information: other information: other information: sequence surviver:
NAME/KEY: allele (SEQ NAME/KEY: allele (SEQ OTHER INFORMATION: (Unaffected) OTHER INFORMATION: /label= 2462
FEATURE:
NAME/KEY: allele
LOCATION: replace(3878, "a")
OTHER INFORMATION: /phenotype= OTHER INFORMATION: (Unaffected)
OTHER INFORMATION: /label= 2462
OTHER INFORMATION: (Unaffected)
OTHER INFORMATION: (Unaffected)
OTHER INFORMATION: (Unaffected)
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5606 TGCCTCCTTTGGTGAAGGTGAAGTGACACTCTGACCTCTTCAGTGACCACTCTACGGTGTC 5665
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                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                      Length 10825;
                                LOCATION: replace(3872, "g")

TOTAE INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                Indels
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APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Truchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TWO NUMBEND and CREW LLP
STREET: TWO Embarcadero Center, 8th Floor
                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
                                                                                                                                                                            99.6%; Score 432.4; DB 3; 99.8%; Pred. No. 3.6e-141; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Two Embarcadero Center, 8th Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTTCTGTTTTAG 434
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                                                                                                                                                                                                                              433; Conservative
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            NAME/KEY: allele
                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-724-394A-20
                                                                                                                               US-09-503-444A-5
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LOCATION: join (361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join (361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION:
OTHER INFORMATION: mutation"
OTHER INFORMATION: mutation"
OTHER INFORMATION: gene 24d2 allele"
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 3852..3891

OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "start and stop positions for
genomic sequence surrounding variant
for 24d1(G) allele (SEQ ID NO:20)"
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Touchift, Roger K.
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8907-0088-999
                                                                                                                                                                                                                                                                                                                                                                                             UPEACHING SYSTEM: WAINGOWS 95
SOFTWARE: Wordberfect Version 8
CURRENT APPLICATION DATA:
PAPPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 2-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: MATCOWS 95
SOFTWARE: WordPerfect Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFRENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: - - 5507..6023
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 5507..602:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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NAME/KEY:
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Pred. No. 2.2e-140;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

LOCATION: 1..246240

OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-20
                                                                                                        017957-000100
               CLASSIFICATION: 536
ATTONNEY AGENT INFORMATION:
NAME: Fitts, Renee A. REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01795
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNES: not relevant
TOPOLOGY: not relevant
MOMERULE TYPE: CDNA
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Best Local Similarity 99.8%;
Matches 433; Conservative
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTTCTGTTTTAG 434
FILING DATE:
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US-08-724-394A-21
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Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Raudy, David A.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston

Kronmil, Gregory S. Lauer, Peter M. Ruddy, David A. Thomas, Winston Tsuchihashi, Zenta Wolff, Roger K.

TITLE OF INVENTION: TITLE OF INVENTION:

APPLICANT: APPLICANT:

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197909 TGCCTCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACACTCTACGGTGTC 197968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 246240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk

COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
RAGELSTRATION NUMBER: 35.136
REGISTRATION NUMBER: 35.136
REGISTRATION NUMBER: 35.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 432.4; DB 2;
Pred. No. 2.2e-140;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

| COCATION: 1..246240

| OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198329 TTTTTCTGTTTTAG 198342
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not relevant
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INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.8
Matches 433; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: not
                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Megabase Transcript Map: No. 5872237el
Sequences and Antibodies Thereto
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198149 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 198208
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LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation: OTHER INFORMATION: mutation: OTHER INFORMATION: gene 24d1 allele" (HH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "start and stop positions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTOTE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Verbion #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGLETRATION UNDRER: 30,223
REFERENCE/DOCKET NUMBER: 17957
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08652265
Patent No. 6025130
                                                                                                                                                                                                                                                                                                            198329 TTTTTCTGTTTTAG 198342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                              TITITICIGITITIAG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION: 140..7319
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Thomas
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                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-652-265-3
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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99.8%; Pred. No. 2.2e-140;
tive 0; Mismatches 1; Indels 0;
                                                                                                                                      APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Touchihashi, Zenta
APPLICANT: Touchihashi, Zenta
APPLICANT: Touchihashi, Zenta
APPLICANT: Touchihashi, Sequences
APPLICANT: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "HLA-H.CONTIG"
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                                                               Sequence 22, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INCRMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELERAM: 415-576-0200
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTER.STICS:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTER.STICS:
TELENGTH: 246240 base pairs
TYPE: nucleic acid
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not relevant
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), LOCATION: 1...246240
; OTHER INFORMATION: /not
US-08-724-394A-22
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ADDRESSEE: TOWNSEND
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MOLECULE TYPE:
                                                   US-08-724-394A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Best Local
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GCTGAGAAAATCTATTGGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA
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ADDRESSEE: Townsend and Townsend and Crew LLI
STREET: Two Embarcadero Center, Eighth Floor
CTTY: San Francisco
STATE: California
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OTHER INFORMATION: /phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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LOCATION: 3852..3891
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LOCATION: 140..7319
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LOCATION: join(361,
LOCATION: 6040.615;
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                  LOCATION: 5507..6023
COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
FRATURE:
FRATURE:
FRATURE:
COTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
FRATURE:
COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d1
US-08-652-265-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.3%; Score 430.8; DB 3; Length 10825; 99.5%; Pred. No. 1.3e-140;
                                             NAME/KEY: -
LOCATION: 3852..3891
LOCATION: Mote= "start and stop positions for OTHER INFORMATION: for genomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
    OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
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APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary I
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Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
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Best Local Similarity 99.5<sup>3</sup>
Matches 432, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drayna,
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APPLICANT:
APPLICANT:
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US-08-652-265-7
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join(361..436, 3762..4025, 4235..4510, 5606..5881, 6040..6153, 7107..7147)
NRMATION: /product= "Hereditary Hemochromatosis
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: CDNA containing a combination of both OTHER INFORMATION: 24dl and 24d2 alleles OTHER INFORMATION: (SEQ ID NO:12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Hereditary Hemochromatosis (Hi
gene containing a combination of both
24d1 and 24d2 alleles"
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LOCATION: 5507..6023

OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: genomic sequence surrounding variant
OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,265
FILING DATE: 3-MAY-1996
CLIASIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STG-0200
TELEPHORE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
IENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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Length 10825;

DB 3;

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5666 GGGCCTIGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725
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OTER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Hereditary Hemochromatosis (HH)
gene 24d1 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..56
LOCATION: 6040..6153, 7107...7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: 3852..3891
LOCATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "start and stop positions for
genomic sequence surrounding variant
for 24d1(A) allele (SEQ ID NO:21)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /note= "start and stop positions OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
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    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= 24d1
                                                            FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POISSARIC, BRIAN M.
REGISTRATION NUMBER: 29,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELERX: 650-493-4935
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: mucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation"
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OTHER INFORMATION:
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NAME/KBY: allele
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LOCATION:
LOCATION:
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NAME/KEY:
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                                                                      1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                            Gaps
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US-08-834-497A-3
i Sequence 3, Application US/08834497A
i Batent No. 6140305
i GENERAL INFORMATION:
i APPLICANT: Thomas, Winston J.
APPLICANT: Reder, John N.
i APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: WUNDIENCES: 76
CORRESPONDENCE ADDRESS:
                            .
0
                         Indels
    99.5%; Pred. No. 1.3e-140;
tive 0; Mismatches 2;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BY PPC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTEM FOR WINDOWS 95
CURENT APPLICATION DATA:
CURENT APPLICATION DATA:
MPDLICATION NOWBER: US/08/834,497A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 04-APR-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
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APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
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Best Local Similarity 99.5
Matches 432; Conservative
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APPLICATION NUMBER: 1
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ZIP: 10036-2811
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5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGGTAATTATGGCAGTGAGA 5965
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                                                                                LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6133, 7107..7147)
OCHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10825,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: replace(3872, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                          and 24d2 mutations"
/note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                       NAME/KEY: -
LOCATION: 140..7319
COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: cDNA containing a combination of both OTHER INFORMATION: 24d1 and 24d2 alleles OTHER INFORMATION: (SEQ ID NO:12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
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99.3%; Score 430.8; DB 3;
Best Local Similarity 99.5%; Pred. No. 1.3e-140;
Matches 432; Conservative 0; Mismatches 2;
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OTHER INPORMATION: /phenotype
OTHER INFORMATION: /label= 24
                     MOLECULE TYPE: DNA (genomic)
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linear
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NAME/KEY:
                                                                 NAME/KEY:
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                                                          241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
                                                                                                                    301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTRY: NGW TOTK
COUNTRY: NGA
ZIP: 10036-2811
COMPUTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENAPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows Version 2.0b
SOFTWARE: FASTENG for Windows Version 2.0b
SOFTWARE: 04-AFR-1997
FLILING DATE: 04-AFR-1997
FLILING DATE: 04-AFR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-AFR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-AFR-1996
CLASSIFICATION: 514
ATTORNEY, AGENT INFORMATION:
NAWE: Poissart Noissart Noissart
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-834-497A-7
; Sequence 7, Application US/08834497A
; Partent No. 6140305
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907.
TELECOMMUNICATION INFORMATION:
TELEPAN: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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STATE: New York
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 5966 TGAGGATCTGCTTTGTTAGGGGGTGGGCTGAGGGTGCAATCAAAGGCTTTAACTTGC
 6025

 Qy
 421 TTTTCTGTTTTAG
 434

 Db
 6026 TTTTTCTGTTTTAG
 6039

Search completed: February 11, 2004, 17:12:26 Job time: 56.7163 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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September 12, 2003, 21:53:18; Search time 109.119 Seconds (without alignments) 6373.435 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 1 atcatgagtgtcgccgt 17 US-09-981-606-30 Scoring table: Title: Perfect score: Sequence:

2888711 seqs, 20454813386 residues Searched: 5777422 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1 AR199266 177 bp DNA linear DEFINITION Sequence 30 from patent US 6355425. ACCESSION AR199266 1 G1:20249340 KEYWORDS 100Known. OVENIUM 100Known. ONCONTENT UNKNOWN. TOTALE 1 (Dassel 1 to 17) AUTHORS Rothenberg B.E., Sawada-Hirai,R. and Barton,J.C. TITLE Mutations associated with iron disorders JUGNRAL Patent: US 6355425. FRATURES Location/oualifiers	PAT 20-APR-2002												
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N N E S J		com patent US 6355425.		1:20249340					0 17)	 Sawada-Hirai, R. and Bar 	sciated with iron disorders	55425-A 30 12-MAR-2002;	:ion/Qualifiers
RESULT 1 LAL19266 LAL19266 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE SOURCE AUTHORS TITLE JOURNAL FEATURES	AR199266	Sequence 30 fr	AR199266	AR199266.1 GI		Unknown.	Unknown.	Unclassified.	1 (bases 1 to	Rothenberg, B.E	Mutations asso	Patent: US 635	Locat
	RESULT 1 AR199266 LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES

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1 (bases 1 to 32)
Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 44 31-OcT-2000;
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1 (bases 1 to 17)

Rothenberg, B. E., Sawada-Hirai, R. and Barton, J. C. Mutations associated with iron disorders

Patent: US 6509442-A 30 21-JAN-2003;

Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0;
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AR275785.1 GI:29709342
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 32)
Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 44 08-MAY-2001;
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               DNA
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Sequence 43 from Patent W00214555.
AX393579
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     32 bp
Sequence 44 from patent US 6228594.
AR149496
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Sequence 11 from Patent W00212557.
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PAT 08-AUG-2001
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I (bases I to 40)
Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D., Tsuchihashi, Z. and Wolff, R.K.
                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 40)
Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 41 31-0CT-2000;
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ive 0; Mismatches 1;
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Pred. No. 1.1e+03;
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Sequence 41 from patent US 6228594.
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AR149493.1 GI:15114084
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Patent: US 6228594-A 43 08-MAY-2001;
Location/Qualifiers
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Best Local Similarity 94.1
Matches 16; Conservative
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                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
                                                                             Wittwer, C.T., Crockett, A.O., Caplin, B.E., Stevenson, W., Wagner, L.A., Chen, J. and Kusukawa, N. Single-labeled oligonucleotide pabes Single-labeled oligonucleotide Pabes Patent: WO 0214555-A 43 21-FEB-2002; University of Utah Research Foundation (US); Idaho Technology,
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 43 31-OCT-2000;
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Sequence 43 from patent US 6228594.
AR149495.1 GI:15114086
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Sequence 43 from patent US 6140305.
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ARI17825.1 GI:14098731
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/db_xref="taxon:9606"
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Matches 16; Conservative
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AR149495
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Umek,R.M.
Sequence determination of nucleic acids using electronic detection
Patent: WO 0107665-A 37 01-FEB-2001;
Clinical Micro Sensors, Inc. (US)
Location/Qualifiers
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mote="taxon:32630"
/note="Synthetic."
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//organism="synthetic construct"
//mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 37 from Patent W00107665.
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Sequence 22 from Patent WO0107665.
AXO80184
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24 c 16 g
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Systems and method for detection assay production and sale Patent: WO 0244994-A B23 06-JUN-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
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Fen endonucleases
Patent: WO 02070755-A 207 12-SEP-2002;
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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KEYWORDS SOURCE

VERSION

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FEATURES

PAT 22-FEB-2001

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Chiu, N. and Jurinke, C.
Methods for generating databases and databases for identifying
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polymorphic genetic markers
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Location/Qualifiers

1. 100
//organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(without alignments)
3527.096 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                              5105512
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                          2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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| SIDSI, gggdata/geneseq.geneseqn.embi.Nal.908.nal.st. /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAp:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Probe for detection	יייייייייייייייייייייייייייייייייייייי	sednence surroundi	Gene fragment which	Himan probe taxed	Company Property	Sequence surround:	DNA fracment with	Oliqonucleotide Dl	
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			Match Length DB		17	32)	30	31	32	40	47	7.5	
	dР	Query	- 1		100.0	100.0		9.06	90.6	9.06	90.6	90.6	9.06	
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Oligonucleotide DI Human HLA-H exon 2 Human polynucieoti DNA encoding beta Hereditary haemoch Human hereditary h Human hereditary h CDNA sequence enco Haemochromatosis g	Hereditary haemoch Human hereditary h Human hereditary h Genomic DNA of a h	Hereditary haemoch Hereditary haemoch Human SCNZA PCR-SS N. gonorrhoeae nuc Human SCNZA genomi N. meningitidis pa Bacillus lichenifo Drosophila melanoq	Drosophila melanog Drosophila melanog Neisseria meningit N. meningitidis B Rat spliced transc Bacillus clausii g Drosophila melanog BAC containing rep	Human probe HHDP2 Human probe HHDP3 Human probe HHDP1 Mutated gene fragm Human probe target Sequence surroundi
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RESU AAA9	RESULT 1 AAA96797
23	AAA96797 standard; DNA; 17 BP.
AC A	AAA96797;
V I X	19-FEB-2001 (first entry)
DE	Probe for detecting histocompatibility iron loading gene mutation 865C.
KKK	Human; histocompatibility iron loading protein; HFE protein; major histocompatibility complex; non-classical class I gene; chromosome 6p; iron disorder; haemochromatosis; probe; ss.
SO	Homo sapiens.
A N N	WO200058515-A1.
4 E \$	05-ocT-2000.
PF	24-MAR-2000; 2000WO-US07982.
Y H	26-MAR-1999; 99US-0277457.
A A A	(BILL-) BILLUPS-ROTHENBERG INC.
PI	Rothenberg BE, Sawada-Hirai R, Barton JC;
DR Y	WPI; 2000-647244/62.
PŢ	Diagnosing an iron disorder e.g. hemochromatosis or a genetic

ALIGNMENTS

| SIDSI/goddata/geneseg/genesegn-embl/NA1983.DAT:* | SIDSI/goddata/geneseg/genesegn-embl/NA1984.DAT:* | SIDSI/gogdata/geneseg/genesegn-embl/NA1985.DAT:* | SIDSI/gogdata/geneseg/genesegn-embl/NA1986.DAT:* | SIDSI/gogdata/genesegn/genesegn-embl/NA1986.DAT:* | SIDSI/gogdata/genesegn/genesegn-embl/NA1986.DAT:* | SIDSI/gogdata/genesegn/genesegn-embl/NA1987.DAT:* | SIDSI/gogdata/genesegn/genesegn-embl/NA1986.DAT:* | SIDSI/gogdata/genesegn-embl/NA1987.DAT:* | SIDSI/gogdata/genesegn-embl/NA1986.DAT:* | SIDSI/gogdata/genesegn-embl/NA1986.DAT:* | SIDSI/gogdata/genesegn-embl/NA1987.DAT:*
Diagnosing an iron disorder e.g. hemochromatosis or a genetic

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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed a having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                               04-APR-1997;
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                                                                                                                       Query Match
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The present sequence represents a probe which is used to detect the brutation S65C in the human histocompatibility iron loading (HFE) protein. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C of missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number 160319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder e.g. haemochromatosis, or a genetic susceptibility to develop it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic
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                                                                                                                   Example 1; Page 29; 55pp; English.
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96US-0652265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATCATGAGTGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-006341/01.
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The present sequence represents a fragment of the gene to which probe ABL539 hybridises. This probe was used to detect the mutation H63D, which is responsible for haemochromatosis. The probe is used to demonstrate the method of the invention. The specification describes a method for detecting a mutation at position in a target nucleic acid by solid phase amplification process. The region of interest is amplified on at least two separate supports (A. B) using at least one primer linked, at its 5'-end, to the supports. The DNA strands are then separated and strands in the suspension removed by washing. Bound DNA sequences are hybridized to a probe, the 3'-end of which hybridizes up to, at most, position n-1. The probe is elongated by colymerase and a nucleotides in the 5' to 3' direction, using a DNA equences. The dNTP* uncleotide derivative (dNTP*) that is resistant to exonuclease. The dNTP* editored derivative (dNTP*) that is resistant to exonuclease. The wild type for support B. Products are digested with an exonuclease so that only probes elongated by dNTP* are not degraded. The supports are then washed and non-degraded probes detected in directly. The method is used to detect mutations associated with
alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutation; solid phase amplification; haemochromatosis; cancer; sickle-cell anaemia; beta-thalassemia; alpha-thalassemia; polymorphism; cystic fibrosis; haemophilia; neurodegeneration; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entire genetic region and for detecting and/or identifying genetically modified organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, especially haemochromatosis; sickle-cell anaemia; alpha or beta-thalassemia; cystic fibrosis; haemophilia; neurodegeneration and cancer. The method is also used to study polymorphisms of gene or an
                                                                                                                                          0; · Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting mutations in nucleic acid, useful e.g. for diagnosing haemochromatosis, by solid phase amplification to incorporate exonuclease resistant nucleotide
                                                                                                  Length 32;
                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene fragment which when mutated causes haemochromatosis.
                                                                                                  DB 22;
                                                          BP; 5 A; 5 C; 11 G; 11 T; 0 other;
                                                                                                                     6.4;
                                                                                                                                          Mismatches
                                                                                                  Score 17;
Pred. No.
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0
                                                                                                  100.0%;
                                                                                                                                                                              1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                                                       10 ATCATGAGTGTCGCCGT 26
                                                                                                                                                                                                                                                                                                                    ABL56391 standard; DNA; 30 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-2001; 2001WO-FR02574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-2000; 2000FR-0010425,
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                   Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200212557-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                          Sequence 32
                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cailloux F,
                                                                                                                                                                                                                                                                                                                                                            ABL56391;
                                                                                                Query Match
                                                                                                                                                                                                                                                                                RESULT 3
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8 X G G
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AAC68461 standard; DNA; 32 BP
                                                                                          AAC68461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC68459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
         RESULT 5
                               AAC68461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a new probe for analysing a target nucleic acid comprising of a fluorescent detecting entity consisting of a single-labelled oligonucleotide having a sequence complementary to a locus of the target nucleic acid and a fluorescent label linked to an internal residue of the oligonucleotide. The probe is useful in melting curve analysis, genotyping, detecting pathogens such as Salmonella, and in determining the presence of a target nucleic acid sequence in a biological sample. This polynucleotide sequence represents a probe target of the invention for melting analysis of haemochromatosis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human probe target HHDT1 of haemochromatosis-associated mutation C187G.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New probe useful for e.g. genotyping, comprises a single-labelled obligonucleotide having a sequence complementary to a locus of the target nucleic acid and a fluorescent label linked to an internal residue of the oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fluorescent detecting entity; melting curve analysis; genotyping; pathogen; probe; human; Factor V Leiden mutation; target; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagner LA;
                                                                 Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.6%; Score 15.4; DB 24; Length 31; larity 94.1%; Pred. No. 51; Conservative 0; Mismatches 1; Indels
                                                                                                            Indels
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                                                               DB 24;
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                  Sequence 30 BP; 6 A; 7 C; 10 G; 7 T; 0 other;
                                                          Score 15.4; DB
Pred. No. 51;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 17; 73pp; English.
                                                                                                        0
                                                               90.68;
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                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-2001; 2001WO-US25231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-224726P.
2000US-240610P.
                                                                                                                                                1 ATCATGAGTGTCGCCGT
                                                                                                                                                                         5 ATCATGAGAGICGCCGT
                                                                                                                                                                                                                                                                                                   AAK98989 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kusukawa N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-269208/31.
                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation C187G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-2000;
16-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2002
                                                                                                     16;
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                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                AAK98989;
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                                                                                                     Matches
                                                                                                                                                                                                                                                                               AAK98989
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having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 90.6%; Score 15.4; DB 22; Local Similarity 94.1%; Pred. No. 51; es 16; Conservative 0; Mismatches 1;
                                                                            HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 32 BP; 6 A; 5 C; 11 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence surrounding HH mutation 24d2 c.
                                        Sequence surrounding HH mutation 24d7a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Column 21; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                      96US-0630912.
96US-0632673.
96US-0652265.
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                                                                                                                                                                                                                                                                97US-0834497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 ATCATGAGAGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC68459 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         (BIRA ) BIO-RAD LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas WJ, Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-006341/01.
                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                              04-APR-1997;
                                                                                                                                                                                                                                                                                                                           16-APR-1996;
23-MAY-1996;
                                                                                                                                                                                                                                                                                                        04-APR-1996;
21-FEB-2001
                                                                                                                                                                                  US6140305-A.
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0;

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Gaps

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Pred. No. 51;

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The specification describes a method for detecting a mutation at a particular position in a target nucleic acid. The method comprises binding the target to a solid support, hybridizing a probe to the target, elongating the probe with howelectide(s) resistant to exonuclease, digesting the probe with exonuclease and detecting bound nucleic acid. The mutation is in position "" in a target nucleic acid and the 3' extremity of the probe hybridises to position "". The method is used to detect gene mutations implicated in disease, particularly hereditary genetic diseases, especially sickle cell annual, alpha and beta thalassemias, cystic fibrosis, hemophilia and genes implicated in cancer. The present sequence represents a DNA fragment which comprises a mutation which is implicated in hemochical and of the method of the
       Detecting mutation in target nucleic acid, useful for detecting hereditary genetic diseases, comprises using chip whose electrical or optical property changes relative to the presence of hybridized probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                      Sequence 47 BP; 7 A; 12 C; 15 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                  Score 15.4; Di
Pred. No. 53;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                  French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                  90.6%;
ilarity 94.1%;
Conservative
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2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                         20 ATCATGAGAGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                         1 ATCATGAGIGICGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF58246 standard; DNA; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                               Example 4; Page 17; 36pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide D1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single surface
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17-MAR-2000;
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                                                                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF58246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
AAF58246/
        δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                         The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA mutation; hereditary genetic disease; sickle cell anemia; thalassemia; cystic fibrosis; haemophilia; cancer; haemochromatosis; ds.
                                                                                                                                              Wolff RK;
                                                                                                                                                                                                         New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with a mutation which is implicated in haemochromatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                            Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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"this base is mutated to G"
                                                                                                                                                                                                                                                                                                                                                                                                                      90.6%; Score 15.4; DB 22;
94.1%; Pred. No. 52;
1ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40 BP; 7 A; 7 C; 13 G; 13 T; 0 other;
                                                                                                                                            Ruddy D,
                                                                                                                                                                                                                                                              Disclosure; Column 20; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                         Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                     96US-0632673.
96US-0652265.
                            97US-0834497
                                                        96US-0630912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001; 2001WO-FR00604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2000; 2000FR-0002614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH78015 standard; DNA; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                           (BIRA ) BIO-RAD LAB INC.
                                                                                                                                         Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag≂
/note=
                                                                                                                                                                               WPI; 2001-006341/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NUCL-) NUCLEICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164945-A2.
                            04-APR-1997;
                                                        04-APR-1996;
                                                                     16-APR-1996;
23-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA fragment
31-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-2001
                                                                                                                                       Thomas WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cailloux F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
mutation
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
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Gaps

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Length 47; Indels

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The present invention provides a database of human samples obtained from healthy individuals which can be used to identify polymorphic genetic markers. Data obtained for the database can be used to sort the samples by parameters such as age, sex and ethnicity. This is useful in linking markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the database of the invention.
                                                                                                           polymorphism; SNP; human; genetic marker; dįsease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebroprotective, nootropic, neuroprotective; antibacterial; virucide, fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerapy; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing a database for identifying polymorphic genetic markers, comprises obtaining data relating to members of a healthy population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 100;
                                                             Human HLA-H exon 2 coding sequence fragment SEQ ID NO: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodi C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 100 BP; 19 A; 22 C; 29 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ping Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and entering the information into a database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.4; DE
Pred. No. 58;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Den Boom D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Page 303; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 105.
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                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0217251.
2000US-0217658.
2000US-0663968.
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94.18;
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             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 94.1
nes 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SEQU-) SEQUENOM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koester H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-273865/28
                                                                                                                                        drug response; ds
                                                                                                                                                                                                                                         WC200127857-A2.
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10-JUL-2000;
19-SEP-2000;
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             12-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jurinke C;
                                                                                                             Database;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Braun A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI63897;
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          NAME OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                     Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 76;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                Sequence 75 BP; 21 A; 24 C; 16 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 76 BP; 21 A; 24 C; 17 G; 14 T; 0 other;
                                                                                             Score 15.4; |
Pred. No. 56;
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.4; | Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 115; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                   ó
                                                                                                                                                                                                                                                      16
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                                                                                                90.6%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.6%;
94.1%;
                                                                                                                                                                                                                                 26-JUL-2000; 2000WO-US20476.
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2000US-0190259.
                                                                                                                                                                                                                                                                                                                    RESULT 9
AAF58231/c
ID AAF58231 standard; DNA; 76
monitoring gene expression.
                                                                                                                                                                                                   1 ATCATGAGTGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide D1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-159728/16
                                                                                                                        Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200107665-A2.
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                                                                                                                                                                                                                                                    32
                                                                                                Query Match
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    20000S-0236367.
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2000US-0236369.
2000US-0236802.
2000US-0237037.
2000US-0237038.
2000US-0237039.
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2000US-0241787.
2000US-0241808.
2000US-0241809.
2000US-0241826.
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2000US-0249207.
2000US-0249208.
2000US-0249209.
2000US-0249210.
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2000US-0251990.
2000US-0254097.
2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
  29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-SEP-2000;
20-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen
     20000S-0214886
20000S-0215135
20000S-0216847
20000S-0216880
20000S-021829
20000S-021829
20000S-0224518
20000S-0224519
20000S-0224519
20000S-0224519
20000S-022514
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2000US-022547
2000US-0225447
2000US-0225757
2000US-0225758
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2000US-0226868
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2000US-0231244.
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2000US-0232397.
2000US-0232397.
2000US-0232397.
2000US-0232399.
2000US-0232400.
2000US-0232400.
2000US-0233400.
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2000US-0235836.
2000US-0236327.
                                    17-JAN-2001; 2001WO-US01309
                                                             31-JAN-2000)
04-FEB-2000
02-FEB-2000)
16-MAR-2000)
11-MAR-2000)
19-MAY-2000)
19-MAY-2000)
19-MAY-2000)
19-MAY-2000)
11-JUL-2000)
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-AUG-2000;
-AUG-2000;
-SEP-2000;
-SEP-2000;
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-SEP-2000;
-SEP-2000;
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            02-AUG-2001
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Laham N;

Rotem-Yehudar R,

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Ehrlich R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                              the invention trained by ARMA 34497—ARMA 5660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemaia, autoimmune thyroditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rhemmatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isohaemias, (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
                                                                                                        The invention relates to human polynucleotides (AAI63803-AAI64012) and
                                                                                                                                                                                                                                                                 (d) wound healing; (e) neurological diseases e.g. cerebral anomal and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iron absorption regulator; intracellular iron absorption; lung injury; haemochromatosis; transfusion; thalassaemia; haemolytic anaemia; chronic infection; transferrin receptor; TfR; brain tumour; cancer; oxidative stress disorder; issue damage; vascular disease; inflammation; atherosclerosis; autoimmune disease; inflammatory condition; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                      New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 596;
                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                               Sequence 596 BP; 133 A; 157 C; 175 G; 126 T; 5 other;
                                                                               664pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Score 15.4; I
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK49917 standard; cDNA; 1317 BP.
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                                                                                                                                                                                                                                                                                                                                                                                          90.6%;
94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 94.1
Matches 16; Conservative
                                                                             SEQ ID NO 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..1317
/*tag=
WPI; 2001-488781/53
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              P-PSDB; AAM43591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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thalassaemias, haemolytic anaemia or chronic infections, and for thalassaemias, haemolytic anaemia or chronic infections, and for delivering a therapeutic to cells that over-express transferrin receptor (TfR) which are preferably lymphocytes or leukocytes, across the bloodbrain barrier. (I) is further useful for treating brain tumour. (I) is also useful for treating oxidative stress disorders resulting in tissue damage e.g. vascular diseases, inflammation, atherosclerosis, as a platform for drug delivery of therapeutic use for cancer, aroimmune diseases and inflammatory conditions. The monochian manifests specific characteristics advantageous for drug delivery systems. It is a soluble, stable and fully conformed protein. It binds specifically to transferrin receptor (TfR) and therefore targets cells that over-express this receptor. If is continuously internalised by the target cells, thus enabling efficient drug delivery. It dissociates from the receptor in the cells, minimising side effects. It negatively requiates iron absorption, reducing growth of undesired cells and preventing lymphocyte activation.

It is not diluted in the blood as is transferrin. It should not induce an immune response since it is a self non-polyment; protein and delivery of announced to content and delivery or content and delivery of announced the correspondent of the content and proper and processed the correspondent of the content and processed to the content and delivery of announced to correspondent and processed to the content and delivery of announced to correspondent and processed the content and delivery of announced to correspondent and processed to the content and delivery or content and delivery of announced to correspondent and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a soluble polypeptide (1) of beta 2 microglobulin (beta2m)/HFE monochain comprising human beta2m (or its analogue or active fragment), linked to alphal-alpha3 domains of human HFE (a central regulator of iron absorption; undefined), or its analogue or active fragment, by a flexible linker peptide, or a functional derivative or salt of (1). (1) is useful for reducing intracellular iron absorption in patients having hereditary haemochromatosis, transfusions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drugs via monochain is expected to overcome drug-resistance since it is a
                                                                                                                                          Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;
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94.1%; Pred. No. 79;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding sequence of beta2m/HFE monochain.
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                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 2; 77pp; English.
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Best Local Similarity 94.1
Matches 16; Conservative
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2002-383192/41.
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                                                                                                                                                                                                                                                                                                          a linker peptide
                                               P-PSDB; AAU80035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss.

Homo sapiens

US6140305-A 31-OCT-2000 97US-0834497

04-APR-1997;

04-APR-1996;

Human hereditary hemochromatosis cDNA

(first entry)

21-FEB-2001

AAC68429;

ВР

AAC68429 standard; DNA; 1440

AAC68429

406 ATCATGAGAGTCGCCGT 422

pp

 Ω Y

1 ATCATGAGTGTCGCCGT 17

Sat Sep 13 19:33:37 2003

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90.6%;
94.1%;
                                                                                                                                                                                             Query Match 90.6
Best Local Similarity 94.1
Matches 16; Conservative
                1066
                                                                         WPI; 1997-512743/47.
P-PSDB; AAW36499.
     414
                                           04-APR-1997;
                                WO9738137-A1
                                                23-MAY-1996;
                                                                                                                                                                                   Therapeutics.
                                                      16-APR-1996;
                                      16-0CT-1997
                                                    04-APR-1996
     variation
                mutation
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This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmid-based CDNA library following identification of the HH locus in the HLA region of chromosome 6. A single mutation (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a chromosomes and in 4% of unaffected chromosomes. It results in a critical disulphide bridge important for secondary structure. The critical disulphide bridge important for secondary structure. The AT96690, the H437 bp CDNA sequence [13] and their 24d1, 24d2 and 24d7, variants; a clonding or expression vector; host cells; a peptide product chosen from the HH gene product, its variants caldiuss of these; an antibody produced using the peptide; a method residues of these; an antibody produced using the peptide; a method caldius of these; an antibody produced using the peptide; a method cash mutation; an annimal madel for the HH disease; metal differentiation factors and therapeutic agents for mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process or vivo or mitigation of injury due to oxidative process or vivo or mitigation of injury due to oxidative process or vivo or mitigation of injury due to oxidative process or product of a nucleic acid sequence as above; and oligonucleotide directed against a transcriptional product of a nucleic acid sequence as above; and oligonucleotide directed against a transcription of the mannal model
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                                                                                                                                                                                                                                                                                                                                                                  "G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
"C to G substitution (24d2 mutation) results in His to Asp substitution"
                                                                                                                                                                                           "A to T substitution (24d7 variant) results in Ser to Cys substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruddy D, Thomas WJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 4; 115pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERC-) MERCATOR GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0652265.
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Tsuchihashi Z, Wolff RK;
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/note=
         /note=
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                                                                                                                                                                                                                                                                                                                Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                            New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 1440;
                                                                                                                                                                                                                                                                                                                Tsuchihashi Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,
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                                                                                                                                                                                                                                                                                                             Thomas WJ, Drayna DT, Gnirke A, Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.4; I
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 4; 108pp; English.
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96US-0652265.
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-006341/01.
                                                                                                                                                                                                                                             16-APR-1996;
23-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2001
                                                                                                                                                                                                                                                                                                                           Feder JN;
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Indels

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0; Mismatches

Length 1440;

Score 15.4; DB 18; Pred. No. 79;

Homo sapiens.

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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                               Wolff RK;
                                                                                                                                                                                                                                                                                                                     New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 90.6%; Score 15.4; DB 22; Length 1440; Best Local Similarity 94.1%; Pred. No. 79; Matches 16; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                               Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;
                                                                                                                                                                                                                                          Thomas WJ, Drayna DT, Gnirke A, Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 4; 108pp; English.
                                                                                                                                          96US-0630912.
96US-0632673.
96US-0652265.
                                                                                                              97US-0834497.
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16-APR-1996;
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                                             US6140305-A
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Search completed: September 12, 2003, 23:52:10 Job time : 14.0108 secs

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BY319883 BY206107 BY202250 BY18570 BY18570 BY18570 BY18570 BY18570 BY185952 BY159932 AA746759 BY159932 AA716759 BY159932 BY159932 BY159932 BY159932 BY1599315 BY1599315 BY1599315 BY1599315 BY1599315 BY1599315 BY1599315 BY1599315 BY1599315 BY1599315 BY1599315 BY1599315 BY1599315 BY1745026 BY745026 BY745026 BY745026

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B1918632 908 bp mRNA linear EST 16-OCT-2001 603176589F1 NIH_MGC_121 Homo saplens cDNA clone IMAGE:5240735 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contract: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI1607 row: a column: 24
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Onpublished
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BI918632.1 GI:16182310
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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BG506985 601861617
CC075265 CSU-K33r,
BY352115 BY352115
                                                September 12, 2003, 23:31:00; Search time 103.933 Seconds (without alignments) 3975.400 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                              45562784
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                               22781392 seqs, 12152238056 residues
                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                    nucleic search, using sw model
                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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CC075265
BY352115
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BE616360 601279161 CA998121 S345A_F10 AY080089 AY080089 BB605399 BB605399

AK088986 AK009581 BE617417 BE901930 BE616360 CA998121 AY080089 BB605399

B12288

AV328885 AV328885 AA787040 k8c05al.f BG637391 SD15386.5

AV328885 AA787040

BG637391

ALIGNMENTS

High quality sequence start; 3

15.4 15.4

us-09-981-606-30.rst

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Gaps

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CSU-K33r.766.SP6 CSU-K33r Aedes aegypti genomic clone CSU-K33r.766, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-3543
Email: enta@tigr.org
Library was provided by Susan Brown and Dennis Knudson at Colorado
State University.
Seq primer: SP6
Class: BAC ends.
    by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

142 c 127 g 165 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Bukaryota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.
End sequencing of Aedes aegypti BACs
Unpublished
Other_GSSs: CSU-K33r,766.T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xxef="taxon:1159"
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47 c 65 g c2 t
                                                                                                                             Length 684;
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100.0%; Pred. No. 4.7e+02
ive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Brendan Loftus
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                                                                                                                                                     /done_lib="Mil.MGC_121"
//ote="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: ECORV (destroyed); RNA source anonymous pool of 3
site_2: ECORV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dr primed and
directionally cloned (ECORV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3:5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NHLMGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 684)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.llol.gov
Plate: LLCM916 row: b column: 06
High quality sequence stop: 469.
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High quality sequence stop: 708.
Location/Qualifiers
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Gaps

ORGANISM

REFERENCE AUTHORS

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CEE | (bases 1 to 344)

RASULARIA, Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,

Yagi, K., Tomaru, Y., Hasegawa, T., Nogami, A., Schonbach, C.,

Gojobori, T., Baldare, J., Hill, D.P., Bult, C., Hume, D.A.,

Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,

Reisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani,

J.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest,

A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,

Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,

Jarvis, E.D., Kanai, A., Kurockikin, I.V., Lee, Y., Lehhard, B., Lyons

King, B.L., Konagaya, A., Kurockikin, I.V., Dev, Y., Lehhard, B., Lyons

Jarvis, E.D., Maltais, L., Marchionni, L., McKenzie, I., Miki,

King, B.L., Romagaya, A., Kurockikin, I.V., Pavan, W.J., Pertea, G.,

Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring

A., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale

A., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale

A., Shimada, K., Sultana, R., Waynshaw-Boris, A., Yanagisawa

A., Sakaume, N., Hirozane-Kishikawa, T., Konno, H., Nakamura

A., Sakaume, N., Sato, R., Washizume, W., Yanagisawa

A., Sakaume, N., Sato, Hayashizame, W., Materston, R., Lander

B.S., Rogers, J., Birney, E., and Hayashizahi, W., Waterston, R., Lander

E.S., Rogers, J., Birney, E., and Hayashizahi, W. Ruter, P. Matue, P. Sasaki, D., Antue, P. Sollon, A. Matue, V., Shiration

A. Nature 420, 563-573 (2002)
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 344)
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                                                                                                                                                                                                               /tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
97 c 96 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                       90.6%; Score 15.4; DB 13;
94.1%; Pred. No. 7.1e+02;
ive 0; Mismatches 1;
                                                  /organism="Mus musculus"
                                                                                  /mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                                                                                                     /clone="L830026007"
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                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,T., Osato,N., Saito,R., Sizuki,H., Yamanaka,I., Kiyosawa,H.,
Yaqi,K., Tomaru,Y., Haseqawa,Y., Nogami,A., Schonbach,C.,
Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
Beisel,K.W., Blake,J.A., Bradt,D., Bult,C., Hume,D.A.,
Gough,J., Garierli,R., Hill,D.P., Hirokawa,V., Chothia,C., Gorbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
Gough,J., Grimmond,S., Gustinctch,S., Hirokawa,N., Jackson,I.J.,
Jarvis,B.D., Konaai,A., Kawaji,H., Kawasawa,Y., Kedaierski,R.M.,
King,B.L., Konaai,A., Warchioni,L., McKenzie,L., Miki,P.A., Majott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,P.A., Majott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,M., Shimmada,K., Sultana,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Redd,J.C., Redd,J.C., Reid,J., Reid,J., Reid,J., Rangle,C.A., Setou,M., Shimmada,K., Sultana,R., Taylor,M., Sanale,R., Yangler,C., Wilmig,L.G., Wynshaw-Boris,R., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
M., Saxazume,N., Saxazu
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
KIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Labbratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
UKL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
T., Imotani,K., Ishia,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
Submission
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Mus musculus
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MEDLINE PUBMED

COMMENT

FEATURES

JOURNAL

TITLE

EST 10-DEC-2002

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Gaps

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Length 325; Indels 4

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P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki, H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., PertovskyN., Pillai,R., Pontlus,J.U., Qi.D., Resole,G., PettrovskyN., Pillai,R., Pontlus,J.U., Qi.D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Reid,J., Ring, B.C., Ringaald,M., Sandelin,A., Scheider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Taylor,M.S., Taskalae,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Rangisawa,M., Yang,I., Yang,I., Vuan,2., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Haydtsu,N., Hirozane-Kishikawa,T., Komo,H., Nakamua,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imoteni,K., Ishii,Y., Itoh,M., Kagawa,T., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,R.S., Nogers,J., Birney,B. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length const
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-reagesc.riken.go.jp,

Mizawa,K., Arimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alizawa,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Free Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Pred. No. 7.3e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
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Best Local Similarity 94.1%;
Matches 16; Conservative
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                                                                                                                                                          Submissional Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of Cap-trapper selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ladaca, L. C. 340, N. Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C. Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons
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                                        Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY210730 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus CDNA clone F730317N09 5', mRNA sequence.
                    Konno, H., Miyazaki, A
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone_lib="RIKEN full-length enriched, B6-derived CD11
+ve dendritic cells"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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             T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J.,
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Pred. No. 7.2e+02;
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (100), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
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Please visit our web site (http://genome.gsc.riken.go.jp)
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Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                        BY327323 RIKEN full-length enriched, synovial fibroblasts Musmusculus cDNA clone L030041G21 5', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishli,Y., Itch,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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TITLE

COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Maus muslais Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basaki,Y. Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomanu,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Golobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Golobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Balake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., Jarvis,B.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., Maltais,L., Martais,L., Martais,L., Martais,L., Martais,L., Martais,L., Martais,L., Martais,L., Martais,L., Martais,L., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Takenaka,Y., Takada,L., Yang,L., Yang,L
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                    prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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BY319883
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/clone_lib="RIKEN full-length enriched, synovial
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    .347
    /organism="Mus musculus"

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/db_xref="taxon:10090"
/clone="L030041G21"
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94.1%;
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Best Local Similarity 94.17
Matches 16; Conservative
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Buman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                   Email: genome-rosigsc.riken.go.jp,

IRE.ihttp://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
A.T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
Submission
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BY206107 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus CDNA clone F730222A16 5', mRNA sequence.
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,E.S., Rogers,J., Birney,E. and Hayashizaki,Y. and Hayashizaki,Y. of the mouse transcriptome based on functional annotation of 60,770 full-length charse. Nature 420, 563-573 (2002)
                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(68C), YoKohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissues were provided by Takashi Ishikawa ( Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="osteoclast-like cell"
/clone_lib="RIKEN full-length enriched, osteoclast-like
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ilarity 94.1%; Pred. No. 7.3e+02;
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/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                   Contact: Yoshihide Hayashizaki
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BY206107.1 GI:26385983
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                                                                                                                                                                                                                                                                                                     Tel: 81-45-503-9222
Fax: 81-45-503-9216
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MAN BINGSON, SERAGOR, Chordata; Craniata; Vertebrata; Buteleostomi; BrEPREY, MANNEYOER, Seragor, Chordatis, Craniata; Vertebrata; Buteleostomi; Bremans, Chordatis, C
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Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogamia, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Ranapin, A., Matsuda, H., Batalov, S., Ouackenbush, J., Schriml, L.M., Ranapin, A., Matsuda, H., Batalov, S., Ouackenbush, J., Schriml, L.M., Ranapin, A., Matsuda, H., Batalov, S., Gustincich, S., Hicker, C.F., Forrest, J.E., Cousins, S., Caasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanaj, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, F.B., Majott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Ming, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Majott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Ming, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Magoshima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Perrovsky, N., Fillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ranachandran, S., Rangel, C.A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sullain, R., Schneider, C., Walming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Sawai, J., Alzawa, T., Maki, K., Sakai, M., Sakazume, N., Sato, K., Shirakawa, T., Rogers, J., Birney, E., and Hayashizaki, Y. Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                      /clone="F730222A16"
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+ve dendritic cells"
106 c 104 g 84 t
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY170353 RIKEN full-length enriched, bone marrow macrophage Musmusculus cDNA clone I830082A04 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                      Length 357;
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Pred. No. 7.4e+02;
---nas 1;
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    .357
    /organism="Mus musculus"

                                                                                                 /db_xref="taxon:10090"
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                                        /mol_type="mRNA"
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Mus musculus
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94.1%;
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Best Local Similarity
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Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library was prepared and sequenced in Mouse Genome Excyclopedia Project of Genome Exploration Research Group in Riken Genome. Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to mission contributed
URL:http://genome.gsc.riken.go.jb/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itch,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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BY202250 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730112A15 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissues were provided by David A. Hume ( Depts. of Biochemistry and Marobiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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macrophage"
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/tissue_type="bone marrow"
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             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence lustering for construction of a nonredundant cDNA library denome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Res. 11 (2), 281-289 (2001)

Division of Experimental Animal Research in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence in Riken contributed to proper denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and sequence denome and se
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakwa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,M., Arakwa,T., Carninci,P., Fukuda,S., Hirozane
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,
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Fax: 81-45-503-9216
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MEDLINE PUBMED JOURNAL

COMMENT

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BASE COUNT

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source

FEATURES

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Mammalia, Eutrinia, Rodentia; Sciulogiachi, Milidac, Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Haseqava, Y., Nogami, A., Schonbach, C., Rube, D.A., Quackenbush, J., Schrill, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brustc, V., Chothia, C., Corban, J.L. B., Cousins, S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, B., Gough, J., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, E.D., Kanai, A., Kuschthin, I.V., Lee, Y., Lehnard, B., Lyons, P.A., Maglott, D.B., Maltais, L., Marchionni, L., McKenzie, L., Milidac, C., Petrovsky, N., Milidac, L., Marchionni, L., McKenzie, L., Milidac, M., Sandelin, A., Schneider, C., Semple, C., Settou, S., Lindach, R., Pohlad, Y., Janada, K., Okido, T., Pavan, W. J., Pettea, G., Petrovsky, N., Pilat, R., Pontius, J. U., Qi, D., Kanadale, S., Rangel, T., Wanner, S., Chneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Youngher, L., Wahlestedt, C., Wang, Y., Wang, I., Yang, I., Wan, Xan, Yang, I., Yang, I., Yang, I., Yang, I., Waki, K., Shinagawa, T., Konno, H., Nakawa, T., Konno, H., Nakawa, Y., Kaders, D., Shinagawa, A., Yasuishi, A., Sakai, K., Sasaki, D., Shibagawa, A., Yasuishi, A., Yashi, Yang, I., Mayazaki, A., Sakai, K., Sasaki, D., Shibagawa, J., Marawa, T., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayshizaki, Y., Andaysis of the mouse transcriptome based on functional annotation of 60, 770 full-length conservation on the conservation of functional annotation of 60, 700.
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Normalization and subtraction of cap-trapper-selected cDNAs to
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                                                                                                                    Gaps
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                              Score 15.4; DB 13
Pred. No. 7.4e+02;
                                                                                                                    0; Mismatches
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                              90.68;
94.18;
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Mus musculus
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-177, 12000)
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                    Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, O 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/tissue_type="bone marrow"
/cell_type="macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Matches 16; Conserv
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Arakawa,T., Kowai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
AM., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Tissues were provided by Dr. John Todd (Dept. of Medical Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addebbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Computer-based methods for the mouse full-length cDNA
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/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, B6-derived CD11
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354
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Matches 16; Conservative
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CREAKLY, Y. FULTON, Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hune, D. A., Ouackenbush, J., Schriml, L.M., Ranapin, A., Matsuda, H., Batdar, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hune, D. A., Baldarelli, E., Dragani, T.A., Fletcher, C.F., Forrest, J. E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Godyh, J., Grimmod, T., Kawaji, M., Hirokawa, N., Jackson, I.J., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lehrad, B., Lyons, P.A., Magashima, T., Numata, K., Okido, T., Pavan, W., Jercase, G., Petrovsky, N., Pillai, R., Portius, J. J., Perfea, G., Petrovsky, N., Pillai, R., Portius, J. J., Reid, J., Reid, J., Red, J., K., Setou, M., Shimada, K., Sultana, R., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takanaka, Y., Taylor, M.S., Tasadale, R.D., Tomita, M., Yanayi, Y., Shinagawa, A., Yasunishi, A., Sakai, Y., Sakai, D., Yasunishi, A., Yoshino, M., Waterston, R., Lander, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waturion annotation of 60,770 full-length cDnas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of Cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-reségsc.riken.go.jp,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Inotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Myazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissues were provided by Takashi Ishikawa ( Department of Surg 2 Yokohama City University 3-9 Fukuura Kanazawa-ku,Yokohama 236-0004 Japan ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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PUBMED
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0209"
/note="Corgan: lung_tumor; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No.196,7716 - Indwyl Institute for Cancer Research)
profiles into the pUC 18 vector: Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=PM4.&t2=PM4-ET0209-151200-003-f07&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 384.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                       Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              PM4-ET0209-151200-003-f07 ET0209 Homo sapiens CDNA, mRNA sequence
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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20202663
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87 q 93 +
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                                                                         BF883952.1 GI:12274078
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                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.1<sup>§</sup>
Matches 16, Conservative
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Fatent No. 650342

GENERAL INFORMATION:
APPLICANT: Rothenberg, Barry E.
APPLICANT: Sawada-Hiral, Ritauko
APPLICANT: Barron. James C.
TILE OF INVENTION UNIMARISE.
FILE REFERENCE: 24065-004 DIV
CURRENT APPLICATION NUMBER: US/09/679,729
CURRENT FILING DATE: 2000-10-040
PRIOR APPLICATION NUMBER: 09/277,457
MUMBER: OF THING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sawda-Hirai, Riisuko
APPLICANT: Sawda-Hirai, Riisuko
APPLICANT: Barton, James C.
TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
FILE REFERENCE: 10653/002001
CURRENT APPLICATION NUMBER: US/09/277,457
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 17
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US-09-677-457-67
US-08-724-394A-21
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US-08-652-265-42
US-09-673-444A-42
US-09-107-532A-3370
US-09-227-3444
US-08-652-265-11
US-08-652-265-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: S65C Mutation US-09-277-457-30
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APPLICANT: Rothenberg, Barry E.
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SEQ ID NO 30
LENGTH: 17
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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APPLICANT: Thomas, will applicant: Thomas, will applicant: Drayna, Dennis T.
APPLICANT: Brader, John N.
APPLICANT: Gillike, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
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                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
CONTRARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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PULING DATE: 04-APR-197
CLASSIPICATION: 514
PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: US 08/632,673
PRIOR APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: US 04-APR-1996
CLASSIFICATION S14
ATTORNEY/AGENT INFORMATION:
NAMME: POLSSANT, BRIAN M.
REGISTRATION NUMBER: 28,46
                                                                                                                                                                                                                                    E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-503-444A~44
; Sequence 44, Application US/09503444A
; Patent No. 6228594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELERIONE: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 44:
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATCATGAGTGTCGCCGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                CITY: New York STATE: New York
GENERAL INFORMATION:
                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-834-497A-44
                                                                                                                                                                                                                                                                STREET:
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                                                                                                     100.0%; Score 17; DB 4; Length 17; 100.0%; Pred. No. 0.75; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INTENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIDUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 17957-000500 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0300 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-834-497A-44; Sequence 44, Application US/08834497A; Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                      Sequence 44, Application US/08652265 Patent No. 6025130 GENERAL INFORMATION:
                                           CTHER INFORMATION: S65C Mutation US-09-679-729-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 ATCATGAGTGTCGCCGT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                           1 ATCATGAGTGTCGCCGT 17
  ORGANISM: Artificial Sequence
                                                                                                            Query Match 100.0
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                            RESULT 3
US-08-652-265-44
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                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
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Length 32; Indels

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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: HEMOLIF, ROGER K.
TITLE OF INVENTION: HERBDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
90.6%; Score 15.4; DB 3; Length 32;
Best Local Similarity 94.1%; Pred. No. 6.8;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                     SCEWALING SISIEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
SECURATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPBEATING SYSTEM: Windows 95
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43, Application US/08834497A; Patent No. 6140395; GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ATCATGAGAGTCGCCGT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATCATGAGTGTCGCCGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2811
                                                                                                                              94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-834-497A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-652-265-43
                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESEBE: Pennie C. T.
STRPEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Feder, Andreas
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Rederitary Hemochromatosis Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8907-0088-999
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 14-Feb-2000
CLASSIFICATION
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-652-265-43; Application US/08652265; Sequence 43, Application US/08652265; Patent No. 6025130; GENERAL INFORMATION: APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 04-Apr-1996
ATTORNEY/ACENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28.462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ATCATGAGTGTCGCCGT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                 CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                               ZIP: 10036
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                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, David
APPLICANT: Tsuchinhashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMONALCATON INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                               8907-0088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.4;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/08/652,265
23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 41, Application US/08652265; Patent No. 6025130
                          NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/POCKET NUMBER: 8907-
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPEX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas, Winston J. Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 ATCATGAGAGTCGCCGT 26
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-09-503-444A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA (genomic) US-08-652-265-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.68;
94.18;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 23-MAY-19
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Thomas
APPLICANT: Drayna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-08-652-265-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Breder, John N.
APPLICANT: Grirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
UNUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DCOKET NUMBER: 8907-0056-999
TELECOMUNICATION INFORMATION:
TELEPRAN: 650-493-4935
TELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1155 Avenue of the Americas CITY: New York COUNTX: USA ZIP: 10036 COMPINE: OR OF THE COUNTY: USA ZIP: 10036
___к: US 08/632,673
16-APR-1996
N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
                                                                                                                APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43, Application US/09503444A Patent No. 6228594
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/632,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ATCATGAGAGTCGCCGT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 90.69
Best Local Similarity 94.19
Matches 16; Conservative
                                 APPLICATION NUMBER: UFILING DATE: 16-APR-1 CLASSIFICATION: 514 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Indels

Mismatches

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16; Conservative

Matches

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Length 40;
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                                                                                                                                                    APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
OWNBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.6%; Score 15.4; DB 3; 94.1%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8907-0088-999
                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordberfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-252-991A-9808/c
; Sequence 9808, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marc J. Rubenfield et al.
                                 Sequence 41, Application US/09503444A Patent No. 6228594 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28,462
                                                                                           APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATCATGAGTGTCGCCGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 ATCATGAGAGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TRNGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 90.6
Best Local Similarity 94.1
Matches 16; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: 212
TELERAX: 6141
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                                                                                                                                                                                                                                                                                                                                                                                                 10036
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              US-09-503-444A-41
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                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                 APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolif, Roger K.
IIILE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTR: New LOLA
COMPUTR: 10036-2811
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows Version 2.0b
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA: US/08/834,497A
FILING DATE: 04-APP-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.6%; Score 15.4; DB 3; Best Local Similarity 94.1%; Pred. No. 7; Matches 16; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: CLASSIFICATION: NATURNEY/AGENT INFORMATION: NAME: Poissant, Brian M. REGISTRATION NUMBER: 28,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 04-APR-1996
CLASSIFICATION DATA:
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                             SSEE: Pennie & Edmonds LLP: 1155 Avenue of the Americas New York
                                                                                                                                 Sequence 41, Application US/08834497A Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 99
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                               APPLICANT: Thomas, Winston J. APPLICANT: Drayna, Dennis T.
                           19 ATCATGAGAGTCGCCGT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATCATGAGTGTCGCCGT 17
1 ATCATGAGTGTCGCCGT 17
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US-08-834-497A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                    US-08-834-497A-41
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STATE:
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90.6%; Score 15.4; DB 3; Length 1440; 94.1%; Pred. No. 12; Live 0; Mismatches 1; Indels 0;
                                                        /phenotype= "normal or wild-type
(unaffected)"
/label= 24d2
                                                                                                                                                               FEATURE:
NAME/KEY: allele
IJOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d7
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: SMITCH, Milliam M.
REGISTRATION NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 6025130
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Greder, John N.
APPLICANT: Greder, John N.
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis General Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of C
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                                           replace(408, "c")
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.65
Best Local Similarity 94.15
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing]
                                                                         OTHER INFORMATION:
                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
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      allele
         NAME/KEY:
LOCATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPECTICS FILE REFERENCE: 10.7196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9808
LENGTH: 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREEF: Two Enbarcadero Center, Eighth Floor STRTY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.6%; Score 15.4; I Best Local Similarity 94.1%; Pred. No. 10; Matches 16; Conservative 0; Mismatches
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1795:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08652265
Patent No. 6025130
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 ATCATGAGTGTCTCCGT 319
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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FEATURE:
NAME/KEY: allele
LOCATION: replace(414, "a")
CTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
..... TWFORMATION: /label= 24d7
                                                                                                                                                                                     /phenotype= "normal or wild-type
(unaffected)"
/label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 90.6%; Score 15.4; I Best Local Similarity 94.1%; Pred. No. 12; Matches 16; Conservative 0; Mismatches
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                                                                                  NAME/KEY: CDS
LOCATION: 222..1268
FEATURE:
NAME/KEY: allele
LOCATION: replace(408, "c")
OTHER INFORMATION: (phenotypeother information: //phenotypeother information: //label= 246
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STRANDEDNESS: single
                      TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: replace
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Gairke, Andreas
APPLICANT: Gairke, Andreas
APPLICANT: Ruddy, David,
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds Lip
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 11036-28H: CORR
ZIP: 11036-28H: Middows Version 2.0b
CORPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
FILING DATE: 04-APR-1997
FILING DATE: 04-APR-1997
PRIOR APPLICATION NAMER: NAME.
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                           . OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis; OTHER INFORMATION: /label= 2441
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NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 314
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
PRIOR APPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08834497A Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                   406 ATCATGAGAGTCGCCGT 422
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TYPE: nucleic acid
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                    222..1268
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Matches 16; Conservat
                      LOCATION:
NAME/KEY:
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DB 3; Length 1440; Indels

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3864.876 Million cell updates/sec
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                                                                                                                                                                            2003, 23:45:10 ; Search time 10.6787 Seconds
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Sequence 6
Sequence 6
Sequence 4
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-142-729-68
US-10-138-888-44
US-10-138-888-77
US-10-138-888-79
US-10-138-888-79
US-10-142-729-67
US-09-927-842-43
US-10-138-888-41
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US-10-138-888-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - nucleic search, using sw model
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                                                                                                                                                                            September 12,
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Maximum DB
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                                                                                                                                                                                  Run on:
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Sequence 27, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 1076, Ap
Sequence 2356, Ap
Sequence 2356, Ap
                                                                                                                           Sequence 40, Appl
Sequence 44, Appl
Sequence 41, Appl
Sequence 207, Appl
Sequence 207, Appl
Sequence 207, Appl
Sequence 2087, Appl
Sequence 1944, Appl
Sequence 1944, Appl
Sequence 144, Appl
Sequence 144, Appl
Sequence 337, Appl
Sequence 337, Appl
Sequence 337, Appl
Sequence 364, Appl
Sequence 364, Appl
Sequence 364, Appl
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Appl
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Sequence 124762,
Sequence 3444, Ap
Sequence 11, Appl
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                    GENERAL INFORMA
                              INFORMA
                                                                                                          Sequence 41, P
Sequence 42, P
Sequence 40, P
                                                                                                  Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide; OTHER INFORMATION: primer US-09-981-606-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                              GENERAL
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Sequence 30, Application US/09981606

Sequence 30, Application US/09981606

Publication No. US20030129595A1

GENERAL INFORMATION:

APPLICANT: Rothenberg et al.

TILLE OF INVENTION: Mutations associated with iron disorders

FILE REFERENCE: 2406-004CON

CURRENT APPLICATION NUMBER: US/09/981,606

CURRENT FILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: 09/277,457

PRIOR APPLICATION NUMBER: 09/277,457

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                     0.5-09-815-242-2087

0.5-09-983-965-5783

0.05-09-983-905-1944

1.05-09-983-802-144

1.05-09-988-802-144

1.05-09-98-075-33

1.05-09-738-075-33

1.05-10-027-632-124762

1.05-09-738-626-3444

1.05-09-738-626-3444
US-09-981-606-1

US-10-108-634A-25

US-10-138-888-1

US-10-138-888-3

US-09-981-666-27

US-10-301-844-2

US-10-301-844-2

US-09-974-300-1076

US-09-974-300-1076

US-09-974-300-1076

US-09-977-842-41

US-09-927-842-44

US-09-927-842-44

US-10-138-888-42

US-10-138-888-42

US-10-138-888-42

US-10-138-207-207-842-44

US-10-138-888-42

US-09-927-842-44

US-10-138-888-42

US-09-927-842-44

US-10-138-888-42

US-09-927-842-44

US-10-138-888-42

US-10-138-207-842-107
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Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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100.0%;
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                                                                                                                    111122111
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Best Local Similarity 100.
Matches 17; Conservative
 2506
5982
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237326
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375
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                                                                                                TYPE: DNA
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RESULT 2
US-10-142-729-68
Sequence 68, Application US/10142729
Publication No. US20030165888a1
GENERAL INFORMATION:
APPLICANT: Brown, Bob D.
APPLICANT: Riley, Timothy A.

9, 7

1440 1440

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Sequence Sequence Sequence Sequence

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APPLICANT: RILEY, TIMOCHY A.

TITLE OF INVENTION: OLICONUCLEOTIDE PROBES AND PRIMERS

TITLE OF INVENTION: OLICONUCLEOTIDE PROBES AND PRIMERS

TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES

TITLE OF INVENTION: OLOGOBAL BASES FOR DIAGNOSTIC PURPOSES

CURRENT APPLICATION NUMBER: US/10/142,729

PRIOR FILING DATE: 2002-08-29

PRIOR FILING DATE: 2001-07-18

PRIOR FILING DATE: 1990-107-18

PRIOR PRIOR DATE: 1990-10-02

PRIOR PRIOR DATE: 1990-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Artificial Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 17; DE Best Local Similarity 100.0%; Pred. No. 5.1 Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 94
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
LENGIH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 1; OTHER INFORMATION: n = modified base US-10-142-729-62
                                                                                               TELECOMMUNICATION INFORMATION:
TELEBHONS: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 62, Application US/10142729
Publication No. US20030165888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 77, Application US/10138888; Publication No. US2030148972A1
GENERAL INFERMATION: APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 ATCATGAGTGTCGCCGT 26
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Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCATGAGTGTCGCCGT
                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-142-729-62/c
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TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
FITE.OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
FILE REFERENCE: OASHIO: 005A
CURRENT TAPLICATION NUMBER: US/10/142,729
FILOR APPLICATION NUMBER: 06/306,229
PRIOR APPLICATION NUMBER: 06/306,229
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: 06/060,673
PRIOR APPLICATION NUMBER: 06/060,673
PRIOR APPLICATION NUMBER: 06/060,673
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 94
SOFTWARE: FASISEO for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wolff, Roger K.
TILE OF INVENTION: Hereditary Hemochromatosis Gene
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FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
FILING DATE: 04-APR-1996
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Artificial Oligonucleotide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Amer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 1, 2
; OTHER INFORMATION: n = modified base
US-10-142-729-68
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44, Application US/10138888 Publication No. US20030148972A1 GENERAL INFORMATION: APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
21P: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATCATGAGTGTCGCCGT 17
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                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-138-888-44
                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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LOCATION: replace(3878, "t")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-884
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
  Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchinashi, Zenta
Wolff, Roger K.
TILLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HH) protein containing the 24d7 mutation"
/note= "Hereditary Hemochromatosis
(HH)gene 24d7 allele"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-AAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 79:
                                                                                                                                                                                                                                                  COMPUTER: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/10142729
Publication No. US20030165888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: -
LOCATION: 5507.,6023
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LOCATION: 140..7319
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                                                                                                                           NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brown, Bob D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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                                                                                                                                                                                                                                                                                                              COMPUTER READBLE Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION CURRENT
APPLICATION DATA:
RELIGION DATA: COMPANIENT OF APPLICATION NUMBER: US/10/138,888
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                             Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Woger K.
OF INVENTION: Hereditary Hemochromatosis Gene
OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
FILING DATE: 04-APR-1996
FILING DATE: 04-APR-1996
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SEQUENCE DESCRIPTION: SEQ ID NO: 77:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-138-888-, GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brian M. Poissant
Drayna, Dennis T.
Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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222..1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                      STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                   ZIP: 10036-2711
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                                                                                                                             TITLE OF NUMBER OF
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US-10-138-888-79
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                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRBUT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brown, Bob D.
APPLICANT: Riley, Timothy A.
TITLE OF INVENTION: OLIGONUCLECTIDE PROBES AND PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-May-2002
CLASSTEICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                              Sequence 43, Application US/10138888 Publication No. US20030148972A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 61, Application US/10142729
Publication No. US20030165888A1
GENERAL INFORMATION:
                                                                                                                                      APPLICANT: Thomas, Winston J.
                                                                                                                                                             Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATCATGAGTGTCGCCGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
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                                     US-10-138-888-43
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                   RESULT 9
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APPLICANT: Crocket, Andrew
APPLICANT: Caplin, Brian
APPLICANT: Stevenson, Wade
APPLICANT: Stevenson, Wade
APPLICANT: Stevenson, Wade
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: MSUKAWA, No. US20030022177Aliko
APPLICANT: MSUKAWA, No. US20030022177Aliko
TITLE OF INVENTION: Sequence Analysis
FILE REPERBUE: 7475-67328
FILE REPERBUE: 7475-67328
FILE REPERBUE: 2001-08-10
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 60/224,726
PRIOR FILING DATE: 2000-10-16
APPLICANT: Riley, Timothy A.

TITLE OF INVERTION: OLICONUCLECTIDE PROBES AND PRIMERS

TITLE OF INVERTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES;
FILE REPERENCE: 0ASBIO.005A

CURRENT APPLICATION NUMBER: US/10/142,729

CURRENT FILING DATE: 2002-08-29

PRIOR PILING DATE: 2001-07-18

PRIOR FILING DATE: 2001-07-18

PRIOR PILING DATE: 2001-07-18

PRIOR PILING DATE: 1998-08-18

PRIOR PILING DATE: 1998-08-18

PRIOR PILING DATE: 1998-08-18

PRIOR PILING DATE: 1998-08-18

NUMBER OF SEQ ID NOS: 94

NUMBER OF SEQ ID NOS: 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.6%; Score 15.4; DB 12; 94.1%; Pred. No. 40;
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94.1%; Pred, No. 41;
1ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Artificial Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: n = modified base US-10-142-729-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43, Application US/09927842 Publication No. US20030022177A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 ATCATGAGAGTCGCCGT
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Best Local Similarity 94.1:
Matches 16; Conservative
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Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1, 2
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                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 67
LENGTH: 21
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APPLICANT: RILEY, TIMOCHY A.
TITLE OF INVENTION: OLIGONUCLECTIDE PROBES AND PRIMERS
TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
FILE REPRENDE: COASBIO: 005A
CURRENT APPLICATION NUMBER: US/10/142,729
CURRENT APPLICATION NUMBER: 00/208-29
PRIOR APPLICATION NUMBER: 00/316,080
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 00/316,080
PRIOR FILING DATE: 1998-08-18
PRIOR PILING DATE: 1998-08-18
PRIOR PILING DATE: 1998-08-18
PRIOR FILING DATE: 1998-08-18
PRIOR PILING DATE: 1998-08-18
PRIOR FILING DATE: 1998-08-18
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                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
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                                    REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Artificial Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.6%; Score 15.4; I Best Local Similarity 94.1%; Pred. No. 42; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.6%; Score 15.4; D 94.1%; Pred. No. 42; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: n = modified base US-10-142-729-63
                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-864
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 206, Application US/09940244; Publication No. US20030044796A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 63, Application US/10142729; Publication No. US/20030165888A1; GENERAL INFORMATION; APPLICANT: Brown, Bob D.
                                                                                                                                                                                                                  LENGTH: 40 base pairs
                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 ATCATGAGAGTCGCCGT 35
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                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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Best Local Similarity 94.1
Matches 16; Conservative
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APPLICANT: Nerl, Bruce
APPLICANT: Hall, Jeff
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TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES FILE REFERENCE: OASBIO.005A
CURRENY APPLICATION NUMBER: US/10/142,729
CURRENY FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/306,229
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 1901-07-18
PRIOR FILING DATE: 1998-08-18
SOFTWARE: FASTSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/M9-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02.10/1138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Artificial Oligonucleotide FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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94.1%; Pred. No. 42;
Live 0; Mismatches
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Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drayna, Dennis T.
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                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity 94.13
Matches 16; Conservative
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19 ATCATGAGAGTCGCCGT 35
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APPLICANT: Hall, Jeff G.
APPLICANT: LUKowiak, Andrew A.
TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences
FILE REFERENCE: FORS-07459
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                           90.6%; Score 15.4; DB 11; Length 46; 94.1%; Pred. No. 42;
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APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
CURRENT APPLICATION NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PatentIn version 3.1
LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE KEEKEKECE: FORS. 0/459,
CURRENT FILING DATE: 2002-11-07
PRIOR FULING DATE: 2002-11-07
PRIOR PELLING DATE: 2002-11-07
PRIOR PILING DATE: 2002-02-27
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2000-11-15
PRIOR PILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: 09/381,212
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PRIOR DATE: 1999-07-09
PRIOR PRIOR DATE: 1996-12-02
PRIOR APPLICATION NUMBER: 08/759,038
PRIOR APPLICATION NUMBER: 08/759,038
PRIOR APPLICATION NUMBER: 08/759,038
PRIOR PILING DATE: 1996-11-26
PRIOR FILING DATE: 1996-07-12
PRIOR FILING DATE: 1996-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 206, Application US/10290386 Publication No. US20030152971A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 ATCATGAGAGTCGCCGT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCAIGAGIGICGCCGI 17
                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 253
SOFWWARE: Patentin version 3.1
SEQ ID NO 206
LENGTH: 46
                                                                                                                                                                                                                                                                                       FEATURE:
; OTHER INFORMATION: Synthetic US-09-940-244-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic US-10-290-386-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lyamichev, Victor
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.1:
Matches 16; Conservative
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-290-386-206
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1 ATCATGAGTGTCGCCGT 17

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LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
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LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                              Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchinabil, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-May-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 9, Application US/10138888
| Publication No. US20030148972A1 | GENERAL INFORMATION: APPLICANT: Thomas, Winston J. | Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brian M. Poissant
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STRANDEDNESS: single
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LOCATION: 222..1268
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                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                CITY: New York
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| NAME/KEY: allele | COCATION: replace(1066, "g") | COCATION: replace(1066, "g") | COTER INFORMATION: /phenotype= "normal or wild-type (unaffected)" | Conaffected)" | Conaffected)" | Conaffected)" | SEQUENCE DESCRIPTION: SEQ ID NO: 9: | Conservation | Second or Seq is a seq is seen to a similarity | Second or Seq is seen in the second of a second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the second or in the seco
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acatcaccatgaagtggctgaaggataagcagocatggatgccaaggggttcgaactctaagagggttt
gcccaatggggatgggcttaccagggetggataaccttggctgtacoccctggggaagagagagagat
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gatttttacacatgtatctatgcattttctggaccogttcaacttttcctttgaatcctctctgtgtt
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tccagacctgaagaatcacaaataattttctacctggtctctccttgttctgataatgaaaattatgataa
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                     APPLICANT: Rothenberg et al.
APPLICANT: Rothenberg et al.
TITLE OF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24055-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
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Sequence 1, Application US/09981606
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tgacetetecectggaactgreteteatgaaccīcaagetgcatetagaggettecttectecege cactecagagacatacacetargteatttecatttecatttetgaagaggaectecttaaatttgggggg etacatgattecattttaacatetggaaagetttgaaceetgggaegtggeragteatacetaece gatttttacacatgtatetatgcattttetggaccegtteaactttecetttgaateetetetgtt tgotgogttcacactctctgcactacctcttcatgggtgcctcagagcaggaccttggtctttccttgtt tgaagctttgggctacgtggatgaccagctgttcgtgttctatgatcatgagagtcgccgtgtggagccc geccaatggggatgggacctaccagggctggataaccttggctgtaccccctgggggaagagcagagatat acgtnccaggtggagcacccaggcctggatcagccctcattgtgatctgggagccctcaccgtctggca ccctagtcattggagtcatcagtggaattgctgtttttgtcgtcatcttgttcattggaattttgttcat gtatgätgggfgtttttagcaggtággaggcaaatatcttgaaaggggttgtgaagägggttttttcta attggcatgaaggtgtcatacagatttgcaaagtttaatggtgccttcatttgggatgctactctagtat ttagaaaagttatgtagaaaaagtaaatgtgatttacgctcattgtagaaaagctataaaaatgaataca attaaagctgttatttaattagccagtgaaaaactattaacaacttgtctattacctgttagtattattg gggatcacatgttcactgttgacttctggactattatggaaaatcacaacacagcaaggagtcccacac cctgcaggtcatcctgggctgtgaaatgcaagaagacaacagtaccgagggctactggaagtacggggtat gatgggcaggaccaccttgaattctgccctgacacactggattggagagcagcagaacccagggcctggc ccaccaagctggagtgggaaaggcacaagattcgggccaggcagaacagggcctacctggagagaggactg acccagtaactcatctgtcaccaagccttggggattcttccatctgattgtgatgtgaggttgcacagcta tgaaggetgtgeaetgeaetggaaggaaggeaeetgteeeagaaaaaageateatgetatetggggta tocagacotgaagaatcacaataattttctacotggtototottgttotgataatgaaaattatgataa tottacaataattotatgagataggtactattatococatttotttttaaatgaagaaagtgaagtagg ccgggcacggtggctcgcgcctgtggtcccagggtgctgagattgcaggtgtgagccaccctgcccagcc tottetttaggeattaaattttageaaagatateteeatetetettetttaaaaeeatttetttttttgtgg atgggcccgcgagccaggccggcgcttctcctcctgatgcttttgcagaccgcggtcctgcaggggcgct cgaactccatgggtttccagtagaatttcaagccagatgtggctgcagctgaggtcagagtctgaaagggt APPLICANT: Rothenberg et al.
TITLE CF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
LENGTH: 2506 Sequence 1, Application US/09981606 GENERAL INFORMATION: ORGANISM: Homo sapiens TYPE: DNA 09981606-1B